

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:10:08 ; Search time 6059.98 Seconds

(without alignments)

3720.338 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVKSGDKPSLSARYV 235

Scoring table:

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YBAPOP 10.0 , YBAPEXT 0.5
FGAPOP 6.0 , FGAPEXT 7.0
DELPO 6.0 , DELEXT 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | ID | Description |
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| 2 | 1247 | 100.0 | 708 | 2 | AX764523 Sequence |
| 3 | 1247 | 100.0 | 773 | 2 | BD226429 Immunosp |

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| 5 | 1247 | 100.0 | 1059 | 2 | CQ725925 | Sequence |
| 6 | 1247 | 100.0 | 1060 | 2 | I23895 | Sequence |
| 7 | 1247 | 100.0 | 1060 | 2 | AR380469 | Sequence |
| 8 | 1247 | 100.0 | 1060 | 5 | HUMATCTBAA | Human sapien |
| 9 | 1247 | 100.0 | 1975 | 5 | HUMTCXAAA | Human T-cel |
| 10 | 1247 | 100.0 | 2261 | 2 | CQ882010 | Sequence |
| 11 | 1247 | 99.8 | 708 | 2 | AX764527 | Sequence |
| 12 | 1241 | 99.5 | 1018 | 5 | AY039664 | Homo sapi |
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| 18 | 1166.5 | 93.5 | 2411 | 2 | DD211089 | TRANSGENI |
| 19 | 1162 | 93.2 | 689 | 2 | DD211094 | TRANSGENI |
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| 21 | 1162 | 93.2 | 1987 | 2 | DD211093 | TRANSGENI |
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ALIGNMENTS

RCT from same provisional

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| DEFINITION | CQ882036 | Sequence 28 from Patent WO2004083404. | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| ACCESSION | CQ882036 | Sequence 28 from Patent WO2004083404. | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| VERSION | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
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| ORGANISM | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| REFERENCE | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| AUTHORS | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| TITLE | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
| JOURNAL | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
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| source | CQ882036.1 | GI:54034749 | 708 bp | DNA | linear | PAT 11-OCT-2004 |
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ORIGIN

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Pred. No.: 6.84e-91 Length: 708
Score: 1247.00 Matches: 235

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x CQ882036 (1-708)

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
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Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
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RESULT 2
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DEFINITION Sequence 40 from Patent WO02102852.
ACCESSION AX764523
VERSION AX764523.1 GI:32258731
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Jakobsen, B.K. and Glick, M.
TITLE Modified CD8 molecule, nucleic acid encoding said molecule, and their therapeutic use
JOURNAL Patent: WO 02102852-A 40 27-DEC-2002;
Avidev Limited (GB)

1
Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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source

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ORIGIN

Alignment Scores:
Pred. No.: 6.84e-91 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x AX764523 (1-708)

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| LOCUS | | 773 bp DNA linear | PAT 17-JUL-2003 |
| DEFINITION | | Immunosuppression by blocking T cell co-stimulatory signal 2 | |
| ACCESSION | BD226429 | (B7/CD28 interaction) | |
| VERSION | BD226429.1 | GI:33036199 | |
| KEYWORDS | JP 2002513568-A/8. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | | | |
| AUTHORS | 1 (bases 1 to 773) | | |
| TITLE | Immunosuppression by blocking T cell co-stimulatory signal 2 | | |
| JOURNAL | | | |
| COMMENT | | | |
| OS | JP 2002513568-A/8 | | |
| PN | JP 2002513568-A/8 | | |
| PD | 14-MAY-2002 | | |
| PF | 30-APR-1999 JP 2000547221 | | |
| PI | 30-APR-1998 GB 9809280.2 | | |
| PR | IAN ROBERT LECHLER, ANTHONY DORLING | | |
| PC | C12N15/02, A61K37/027, A61K31/7052, A61K35/14, A61K38/00 PC | | |
| PC | A61K39/395, A61K39/395, | | |
| PC | A61K48/00, A61P37/06, A61P43/00, C07K14/705, C07K16/28, C12N5/10, | | |
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| PC | A61K37/02, C12N5/00 | | |
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| CC | interaction) | | |
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| Db | 97 | CCGAGCCAGTTCCGGGTGTCGGCGTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG | 156 |
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| Db | 217 | CGCGGCGCGCGCCAGTCCCACTTCTCTTATACCTCTCCAAAACAGCCGAGGCG | 276 |
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| Qy | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
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| Db | 397 | TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCCAGCGAAGCCACGACGACG | 456 |
| Qy | 141 | ProAlaProArgProProProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| Db | 457 | CAGGCGCCGACCAACACCGCGCCCACTCGCTCGAGCCCTGTCCTCCCTGCGC | 516 |
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| Db | 697 | GTGGTCNAATCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTC | 741 |
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| AX011079 | | | |
| LOCUS | AX011079 | 773 bp DNA linear | PAT 06-SEP-2000 |
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| ACCESSION | AX011079 | | |
| VERSION | AX011079.1 | GI:9997709 | |
| KEYWORDS | | | |
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| | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | |
| | Hominidae; Homo. | | |
| REFERENCE | | | |
| AUTHORS | 1 | | |
| TITLE | Dorling, A. and Lechler, I.R. | | |
| JOURNAL | Immunosuppression by blocking t cell co-stimulation signal 2 | | |
| | (b7/cd28 interaction) | | |
| | Patent: WO 9957266-A 16 11-NOV-1999; | | |
| | IMP COLLEGE INNOVATIONS LTD (GB); DORLING ANTHONY (GB); LECHLER IAN | | |
| | ROBERT (GB) | | |
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| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 7 42e-91 | Length: | 773 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |
| US-10-804-763-1 (1-235) x AX011079 (1-773) | | | |
| Qy | 1 | MetaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg | 20 |
| Db | 37 | ATGGCTTACAGTACCGCCCTTCTCTCGCGCTGGCTTCTCTCCACCGCCGAGG | 96 |
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| Db | 97 | CCGAGCCAGTTCCGGGTGTCGGCGTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG | 156 |
| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 157 | CTGAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCACGCGG | 216 |
| Qy | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
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Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 457 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGCGCCCTGTCTCGGC 516
Qy 161 ProGluLacCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 517 CCAGAGGCGTCCGCGCAGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTCGCC 576
Qy 181 CysAspileTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 577 TGTGATATCATCTTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTG 636
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 637 GTTATCACCTTTACTGCAACACACAGGAACGAGAGCGTGTTCGAATGTCCCGGCT 696
Qy 221 ValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 697 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 741

RESULT 5
LOCUS CQ725925 1059 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 11859 from Patent WO02068579.
ACCESSION CQ725925
VERSION CQ725925.1 GI:42287423
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 11859 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..1059
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

No

ORIGIN
Alignment Scores:
Pred. No.: 9,94e-91 Length: 1059
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0
US-10-804-763-1 (1-235) x CQ725925 (1-1059)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 65 ATGGCTTACAGTAGACCGCTTCTCTCGCGTGGCTTGTCTCCAGCGCCAGG 124
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 125 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 184
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 185 CTGAAGTCCAGGTCGTCTCCAAACCGACGTCGGCTCTCTGTGGCTCTTCCAGCGC 244
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 245 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAACCAAGCCAGCGG 304
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 305 GCCGAGGGCTGGACACCCAGCGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCTCCTC 364
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 365 ACCCTGAGCGACTTCCCGCGGAGAGAGGGCTACTATTCTCTCGGCCCTTGAGCAAC 424
Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 425 TCCATCATGTACTTCCAGCACTTCGTGCGGCTCTTCTGCGAGCAAGCCACCGACG 484
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 485 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGCGAGCCCTGTCTCGGC 544
Qy 161 ProGluLacCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 545 CCAGAGGCGTCCGCGCAGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTCGCC 604
Qy 181 CysAspileTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 605 TGTGATATCATCTTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 664
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 665 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTTGTTGCAAAATGTCCCGGCT 724
Qy 221 ValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 725 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 769

RESULT 6


LOCUS I23895 1060 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 11 from patent US 5540926.
ACCESSION I23895
VERSION I23895.1 GI:1603765
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 11 30-JUL-1996;
FEATURES Location/Qualifiers
source 1..1060
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:

No

| Pred. No.: | 9,95e-91 | Length: | 1060 |
|------------------------|----------|---------------|------|
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

| US-10-804-763-1 (1-235) x I23895 (1-1060) | |
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| Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20 | |
| Db 66 ATGGCTTTACCACTGACCGCCTTGTCTCTGCGCTGGCTTGTCTCTCACGCCGCGAG 125 | |
| Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40 | |
| Db 126 CCGAGCCAGTTTCGGGGTGTCCCGCTGGATCGAAGCTGGAACTCGGGCGAGACAGTGGAG 185 | |
| Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60 | |
| Db 186 CTGAAGTCCAGGTCTCTGTCTCAACCCGAGCTCGGGCTGTCTGTGGGTCTTCACAGCCG 245 | |
| Qy 61 ArgGlyAlaAlaAserProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80 | |
| Db 246 CGCGGCGCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACAGGCCAAGGCG 305 | |
| Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100 | |
| Db 306 GCCAGGGGGCTGGACACCCAGCGGTCTTCGGCAAGAGGTTGGGGACACCTTCGTCTCTC 365 | |
| Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120 | |
| Db 366 ACCCTTGAGCGACTTCCGCCGAGAGAACGAGGGCTACTATTCTGTCTGCGCCCTGAGCAAC 425 | |
| Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140 | |
| Db 426 TCCATCATGTACTTCAGCCACTTCTGTGCGGTCTTCTTCCAGAGCGAAGCCACACGAGC 485 | |
| Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160 | |
| Db 486 CCAGCGCGCGACACCAACACCGCGCGCCACCATCGCGTTCGACGCGCCCTGTCTCTGCGC 545 | |
| Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180 | |
| Db 546 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGGAGTGACACAGAGGGGGGTGGACTTCGCG 605 | |
| Qy 181 CysAspileTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200 | |
| Db 606 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTCTCTCTGTACTG 665 | |
| Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220 | |
| Db 666 GTTATCACCTTTACTCAACACACAGAGAACCCGAGACGTGTTTGCATAATGTCCTCCGCG 725 | |
| Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235 | |
| Db 726 GTGGTCAAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 770 | |

| RESULT 7 | |
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| LOCUS AR380469 | 1060 bp DNA linear PAT 18-DEC-2003 |
| DEFINITION Sequence 1014 from patent US 6607879. | |
| ACCESSION AR380469 | |
| VERSION AR380469.1 | GI:40088103 |
| KEYWORDS | |
| SOURCE Unknown. | |
| ORGANISM Unknown. | |
| REFERENCE 1 (bases 1 to 1060) | |
| AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J. | |
| TITLE Compositions for the detection of blood cell and immunological response gene expression | |
| JOURNAL Patent: US 6607879-A 1014 19-AUG-2003; Incyte Corporation; Palo Alto, CA | |



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Littman,D.R., Thomas,Y., Maddon,P.J., Chess,L. and Axel,R.
The isolation and sequence of the gene encoding T8: a molecule defining functional classes of T lymphocytes

TITLE

Cell 40 (2), 237-246 (1985)

JOURNAL

PUBMED

3871356

COMMENT

Original source text: Human peripheral T cell, cDNA to mRNA, clones pT8.B and pT8.F1.

FEATURES

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66..773
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VLLSNPTSGCSHLFQPRGAASPTFLYLSQNKPKAAEGLDTQFSKRLGDTFVLT
SDFRRENGYVFCGALNSIMYFHFVFLPAKPTTTPAPRPTTPTPTIASQPLSLR
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66..125
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126..770
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Pred. No.: 1.77e-90 Length: 1975
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x HUMTCXAAA (1-1975)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 88 ATGGCCTTACCAGTACCGCTTGTCTCGCGCTTGTCTTCCACGCGCGCAGG 147
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 148 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAAACCTGGCGGAGACAGTGGAG 207
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 208 CTGAAGTGCAGGTGTCTGTCTCAACCGACGTCGGGCTGTCTGGTCTCTTCCAGCCG 267
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLysSerGlnAsnLysProLysAla 80
Db 268 CGCGGGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCG 327
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 328 GCCGAGGGGCTGGACACCGCGGTTCGGGCAAGAGGTGGGGGACACCTTCGTCTCTC 387
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 388 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGGTACTATTCTGCTCGGCCCTTGAGCAAC 447
QY 121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 448 TCCATCATGTACTTACGCCACTTCGTGCGGCTTCTGCGCAGCGAAGCCACCGACG 507
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 508 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCTCTGCGCG 567
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 568 CCAGAGCGGTGCGGCGCAGCGGGGGCGAGTGCACACGAGGGGGTGGACTTCGCG 627
QY 181 CysAspIleTyTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 628 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTGTCTCCTG 687
QY 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 688 GTTATCACCCTTTACTTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCGCCG 747
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
Db 748 GTGGTCAATCGGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 792

RESULT 10
CQ882010 2261 bp DNA linear PAT 11-OCT-2004
LOCUS Sequence 2 from Patent WO2004083404.
DEFINITION CQ882010
ACCESSION CQ882010
VERSION CQ882010.1 GI:54034736
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE Qi, Y., Zhang, X. and Konigsberg, P. J.
AUTHORS Gene therapy vectors having reduced immunogenicity
TITLE Patent: WO 2004083404-A 2 30-SEP-2004;
JOURNAL

See primly to 3000
provisional
app.

Isogenis, Inc. (US)
Location/Qualifiers
1. .2261
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FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 2.01e-90 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x CQ882010 (1-2261)

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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAAACCTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGTCTGTCTCAACCGACGTCGGGCTGTCTGGTCTCTTCCAGCCG 239
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLysSerGlnAsnLysProLysAla 80
Db 300 CGCGGGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCGCGGTTCGGGCAAGAGGTGGGGGACACCTTCGTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGGTACTATTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTACGCCACTTCGTGCGGCTTCTCTGCGCAGCGAAGCCACCGACG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCTCTGCGCG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGGTGCGGCGCAGCGGGGGCGAGTGCACACGAGGGGGTGGACTTCGCG 659
QY 181 CysAspIleTyTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTGTCTCCTG 719
QY 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCTTTACTTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCGCCG 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
Db 780 GTGGTCAATCGGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 824

RESULT 11
AX764527
LOCUS Sequence 44 from Patent WO20102852.
DEFINITION AX764527
ACCESSION AX764527
VERSION AX764527.1 GI:32258735
KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Jakobsen,B.K. and Glick,M.
TITLE Modified CD8 molecule, nucleic acid encoding said molecule, and their therapeutic use
JOURNAL Patent: WO 02102852-A 44 27-DEC-2002;
Avidev Limited (GB)
FEATURES Location/Qualifiers
source 1..708
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CDS 1..708
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ORIGIN
Alignment Scores:
Pred. No.: 1.19e-90 Length: 708
Score: 1244.00 Matches: 234
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.6% Mismatches: 0
Query Match: 99.8% Indels: 0
DB: 2 Gaps: 0
US-10-804-763-1 (1-235) x AX764527 (1-708)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGGACCTGGAACCTGGCGGAGACGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCGAGTCCGGGCTGCTGCTGCTCTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 CGCGAGGGGCTGGACACCGAGCGGTCTCGGGCAGAGGTGGGGACACCTTCGTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCGCGCTTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGGCACCTTCGTCGGCTTCCTGCCAGCGAAAGCCACCGAGCG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCG 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGGCGTCCG 540

QY 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCCCTTCTCTGTCACTG 600
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCTTTACTGCAACACGAGACGAGCGTGTTCGAATGTCCCGGCGCT 660
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAAGCCAGCGCTTTCGGCGAGATACGTC 705
RESULT 12
AY039664
LOCUS Homo sapiens mutant CD8 alpha antigen (CD8A) mRNA, complete cds.
DEFINITION
ACCESSION AY039664
VERSION
KEYWORDS AY039664.1 GI:14861039
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; EUTHERIA; EUARCHONTGLIRES; PRIMATES; CATARRHINI;
HOMINIDAE; HOMO.
REFERENCE 1 (bases 1 to 1018)
AUTHORS de la Calle-Martin,O., Hernandez,M., Ordi,J., Casamitjana,N.,
Arostegui,J.I., Caragol,I., Ferrando,M., Labrador,M.,
Rodriguez-Sanchez,J.L. and Espanol,T.
FAMILIAL CD8 DEFICIENCY DUE TO A MUTATION IN THE CD8 ALPHA GENE
J. Clin. Invest. 108 (1), 117-123 (2001)
11435463
REFERENCE 2 (bases 1 to 1018)
AUTHORS Casamitjana,N., Arostegui,J.I. and de la Calle,O.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Immunohematology, Centre de Transfusio i
Banc de Teixits, Pg. de la Vall d'Hebron 119-129, Barcelona 08035,
Spain
FEATURES Location/Qualifiers
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Pred. No.: 2.91e-90 Length: 1018
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Query Match: 99.5% Indels: 0
DB: 5 Gaps: 0
US-10-804-763-1 (1-235) x AY039664 (1-1018)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Nothing to suggest


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Db      180 ATGGCTTACCACTGACCGCTTGTCTCTGCGCTGGCTTGTCTCCACGCGCGCCAG 239
QY      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      240 CCGAGCGAGTTCGGGTGTCCGCTGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 299
QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      300 CTGAAGTGGCAGGTGCTGTGTCCAAACCCGACGTCGGGTGCTGTGGCTCTTCCAGCGG 359
QY      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrieuSerGlnAsnLysProLysAla 80
Db      360 CGCGGCGCGCGCCAGTCCACCTTCTCCTATACCTCTCCAAACCAAGCCCAAGGCG 419
QY      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLeuArgLeuGlyAspThrPheValLeu 100
Db      420 GCGAGGGGCTGCACACCCAGCGGTCTCGGCGAAGGTTGGGGGACACTTCGTCTCCTC 479
QY      101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db      480 ACCCTGAGCGACTTCGCGGAGAGAACGAGAGCTACTATTCTGCTCGGCCCTTGAGCAAC 539
QY      121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      540 TCATCATGTACTTACGCGCACTTCGTGCGCGGTCTCTCGCAGCAAGCCACACGACG 599
QY      141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      600 CCAGCGCCCGGACCCACCAACCGCGGCCACCATCGCTCGGAGCCCTGTCTCTGCGC 659
QY      161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db      660 CCAGAGCGCTGCGCGCCAGCGGGGGCGGCGAGTGCACACAGAGGGGGCTGAGACTTCGCC 719
QY      181 CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db      720 TGTGATATCTACATCTGGCGCGCCCTCGCGCGGACTTGTGGGTCTCTCTCTGTCTGCTG 779
QY      201 ValIleThrLeuTyrcysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db      780 GTTATACCCCTTACTTGCACACACAGAACCGAAGACGTGTTCGAAATGTCCCGCGCCT 839
QY      221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
Db      840 GTGGTCAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 884

RESULT 13
BC025715
LOCUS
DEFINITION
Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript
variant 1, mRNA (cdna clone MGC:34614 IMAGE:5227906), complete cds.
ACCESSION
BC025715
VERSION
BC025715.1 GI:19344021
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 2150)
Krausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,I., Max,S.I., Wang,J., Hsieh,F.,
Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.D., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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TITLE
JOURNAL
PUBMED
12477932
REFERENCE
2 (bases 1 to 2150)
Strausberg,R.
Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E.B. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E.B. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 49 Row: 0 Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 2786641.
FEATURES
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/lab_host="DH10B"
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/db_xref="MIM:186910"
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ORIGIN

Alignment Scores:

Pred. No.: 1,01e-89 Length: 2150
Score: 1238.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.3% Indels: 0
DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x BC025715 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 6 ATGGCTTACAGTGACCGCTTCTCTCGCTGGCTTGTCTCCAGCGCCGAGG 65
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 66 CCGAGCCAGTTCCGGGTCTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAG 125
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGGTGCTGCTCCAAACCGGACGTCGGGCTGCTCGTGGCTCTTCCAGCGG 185
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGGCGCGCGCGGACGCTTCTCTATACCTTCTCCAAAACACAGCCCAAGCGG 245
Qy 81 AlaGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 246 GCCGAGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCTGCTC 305
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTrpPheCysSerAlaLeuSerAsn 120
Db 306 ACCCTGAGCGACTTCCGCGAGAGAACGAGGGCTGTATTTCTGCTCGGCGCTGAGCAAC 365
Qy 121 SerileMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 366 TCCATCATGTACTTCAGCACCTTCTGCGCGGTCTCTCCGAGCGAAGCCCAACGACG 425
Qy 141 ProAlaProArgProProThrProAlaProThrileAlaSerGlnProLeuSerLeuArg 160
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Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
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Qy 181 CysAspIleTyrrileTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
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Qy 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
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RESULT 14

CQ843147 CQ843147 3048 bp DNA linear PAT 02-AUG-2004
LOCUS Sequence 1794 from Patent EP1440981.
DEFINITION CQ843147
ACCESSION CQ843147
VERSION CQ843147.1 GI:50894934

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
Yanamoto, J., Isono, Y., Nagai, K. and Irie, R.

TITLE

JOURNAL Full-length human cdna
Patent: EP 1440981-A 1794 28-JUL-2004;
Research Association for Biotechnology (JP)

FEATURES

source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 2,03e-89 Length: 3048
Score: 1236.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.1% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x CQ843147 (1-3048)

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 1092 CCGAGCCAGTTCCGGGTCTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAG 1151
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 1152 CTGAAGTCCAGGTGCTGCTGCTCCAAACCGGACGTCGGGCTGCTGCTGCTTCCAGCGG 1211
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 1212 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAGCCCAAGCGG 1271
Qy 81 AlaGlyLeuAspPheArgGluAsnGluGlyTrpPheCysSerAlaLeuSerAsn 100
Db 1272 GCCGAGGGGTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCTGCTC 1331
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTrpPheCysSerAlaLeuSerAsn 120
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Qy 121 SerileMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 1392 TCCATCATGTACTTCAGCCACTTCTGCGCGGTCTTCTCTCCAGCGAAGCCCAACGACG 1451
Qy 141 ProAlaProArgProProThrProAlaProThrileAlaSerGlnProLeuSerLeuArg 160
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Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
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Qy 181 CysAspIleTyrrileTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
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RESULT 15

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LOCUS Homo sapiens cDNA FLJ42162 fis, clone THYMU2005303, highly similar
DEFINITION to T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR.

AK124156
 AK124156.1 GI:34529876
 oligo capping; fis (full insert sequence).
 SOURCE
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1
 Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
 Sugiyama, T., Irie, Y., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
 Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
 Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M.,
 Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
 Takanashi-Fujii, A., Ohima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
 Sugano, S., Nagahara, K., Masuho, Y., Nagai, K. and Isogai, T.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3048)
 Isogai, T. and Yamamoto, J.
 Direct Submission
 Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan
 (E-mail: flj-cdna@nifty.com, Tel:81-438-52-3975, Fax:81-438-52-3986)
 NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction: Helix Research Institute (HRI) (supported by Japan
 Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
 HRI, and Biotechnology Center, National Institute of Technology and
 Evaluation; clone selection for full insert sequencing: HRI and
 RAB; annotation: Reverse Proteomics Research Institute, HRI and
 RAB.

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ORIGIN
 Alignment Scores:
 Pred. No.: 2.03e-89 Length: 3048
 Score: 1236.00 Matches: 234
 Percent Similarity: 99.6% Conservative: 0
 Best Local Similarity: 99.6% Mismatches: 1
 Query Match: 99.1% Indels: 0
 DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x AK124156 (1-3048)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
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 Db 1092 CCGAGCCAGTTCGGGGTGTCCGCTGGATCGACCTGGACCTGGGACGAGCAGTGGAG 1151
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 1152 CTGAAGTGCAGGTGCTGTGTCCAAACCCAGCTCGGGTCTGCTGGCTCTTCCAGCG 1211

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 29, 2006, 22:39:21; Search time 904.723 Seconds

(without alignments)
2716.542 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
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-YGAPOP=10 -YGAPEXT=0.5 -DEPOP=6 -DSEXT=7

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- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 1247 | 100.0 | 708 | 8 | ABZ69260 Human CD8 |
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| | | | | | |
|----|--------|-------|------|----|----------|
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| 15 | 1247 | 100.0 | 2261 | 14 | ADM86779 |
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| 18 | 1236 | 99.1 | 3048 | 8 | ABZ69262 |
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| 20 | 1149.5 | 92.2 | 2134 | 12 | ADQ22926 |
| 21 | 1132 | 90.8 | 662 | 12 | ADN11772 |
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| 24 | 1108.5 | 88.9 | 4392 | 14 | ADN96283 |
| 25 | 1094 | 87.7 | 708 | 13 | ADS92815 |
| 26 | 1094 | 87.7 | 708 | 13 | ADS19461 |
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| 28 | 1008.5 | 80.9 | 597 | 13 | ADS19441 |
| 29 | 1006.5 | 80.7 | 2150 | 13 | ADS92793 |
| 30 | 1006.5 | 80.7 | 2150 | 13 | ADS19439 |
| 31 | 1006.5 | 80.7 | 2150 | 14 | ADZ26403 |
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| 33 | 954 | 76.5 | 1131 | 3 | AAZ46253 |
| 34 | 937.5 | 75.2 | 3476 | 14 | ADN96284 |
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| 36 | 809 | 64.9 | 785 | 13 | ADS19457 |
| 37 | 792 | 63.5 | 3407 | 14 | ADN96285 |
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| 40 | 708.5 | 56.8 | 2001 | 13 | ADS19453 |
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| 45 | 617 | 49.5 | 1891 | 13 | ADS92809 |

ALIGNMENTS

RESULT 1

AAX80967
ID AAX80967 standard; cDNA; 708 BP.

AC AAX80967;

DT 18-AUG-1999 (first entry)

DE Human CD8 alpha protein encoding cDNA.

KW T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;
KW corticosteroid; human; CD8 alpha protein; ss.

OS Homo sapiens.

PN WO921576-A1.

PD 06-MAY-1999.

PF 28-OCT-1998; 98WO-GB003235.

PR 28-OCT-1997; 97GB-00022779.

PA (ISIS-) ISIS INNOVATION LTD.

PI Jakobsen BK, Gao GF, Gerth UC, Sewell AK;

Submit form
No

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XX DR WPI; 1999-385058/32.
XX DR P-PSDB; AAY21688.
XX PT Inhibiting activity of T cells against target cells useful for treating
XX PT autoimmune diseases and allergy.
XX PS Disclosure; Fig 1A; 79pp; English.
XX SS
XX CC The invention describes a method for inhibiting activity of T lymphocytes
XX CC against a target cell by treating the cell with a soluble form of a CD8
XX CC molecule. The method is used as immunosuppressive therapy, e.g. in
XX CC patients undergoing transplantation, but also for treating autoimmune
XX CC diseases and allergy, e.g. exacerbation of asthma caused by viral
XX CC infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
XX CC vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment
XX CC with CD8 protein provides more selective immunosuppression than use of
XX CC corticosteroids. The present sequence represents a cDNA encoding a human
XX CC CD8 alpha protein
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x AAX80967 (1-708)
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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGGTTCGGCGTGGATCGGACCTGGAACTGGGGGAGACAGTGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTCTCTGTCTCCAAACCGAGCTCGGGCTGCTGTGGCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCCAGTCCACCTTCTCTATATACCTTCTCCAAACAGCCCAAGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCTTGAGCAAC 360
QY 121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCGAAGCCACACGAGG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGCGACCAACACCGCGGCCACCATCGGTGTCGACGCCCTGTCCCTGGGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGGGTGCGCGCCAGCGCGGGGCGGCGAGTGCACACAGGGGGCTGGACATCGCC 540
QY 181 CysAspIleTyTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGGCGGCTTGGCGGGACTTGTGGGGTCTTCTTCTCTGTCACTG 600
QY 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220

601 GTTATCACCTTTACTGCAACCAACAGGAACGAGACGTGTTCGAATGTCCTCCGCGCT 660
221 ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 235
661 GTGGTCAATCGGAGACACAGCCAGCCTTTTCGGGAGATACGTC 705

RESULT 2
ABZ69260
ID ABZ69260 standard; DNA; 708 BP.
XX AC ABZ69260;
XX DT 11-AUG-2003 (first entry)
XX DE Human CD8alpha chain coding sequence.
XX KW Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;
XX KW antiallergic; cytotoxic T cell response; inhibitor; gene; ds.
XX OS Homo sapiens.
XX PN WO2002102852-A2.
XX PD 27-DEC-2002.
XX PF 14-JUN-2002; 2002WO-GB002743.
XX PR 14-JUN-2001; 2001GB-00014533.
XX PA (AVID-) AVIDEX LTD.
XX PI Jakobsen BK, Glick M;
XX DR WPI; 2003-167488/16.
XX DR P-PSDB; AAO19807.
XX PT New modified CD8 molecule having enhanced binding to major
XX PT histocompatibility complex, and having a Serine53 of at least one CD
XX PT alpha chain is mutated to another amino acid, useful for treating e.g.
XX PT graft rejection or hypersensitivity.
XX PS Disclosure; Fig 1A; 60pp; English.
XX CC The present invention provides modified human CD8 molecules whose binding
XX CC to major histocompatibility complex (MHC) is enhanced compared to wild
XX CC type CD8. The modified CD8 molecule or a corresponding nucleic acid is
XX CC useful in medicine, particularly in manufacturing a medicament for
XX CC modulating CD8+ T cell response. The modified CD8 proteins and nucleic
XX CC acids encoding such proteins are useful in immunosuppressive therapy,
XX CC particularly as inhibitors of cytotoxic T cell responses, and for
XX CC treating autoimmune disorders, hypersensitivity (e.g. allergic reaction),
XX CC graft versus host disease, or graft rejection. The present sequence is a
XX CC CD8 coding sequence
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-804-763-1 (1-235) x ABZ69260 (1-708)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACAGTACCGCTTGTCTCTGGCTGGCTTGTCTTCCACGCGCCAGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
```


Db 481 CCAGAGGGCTCCGGCGCAGCGCGGGGGCGCAGTGCACAGAGGGGCTCGACTTCGCC 540
Qy 181 CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCCCTTGGCCGGACTTGTGGGTCCTTCTCTGTCACTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCCCTTTACTGCAACACAGGAAACGAAAGACGTGTTTGCATATGTCCTCCGCGCT 660
Qy 221 ValValIysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 705

RESULT 4

ADSI19462
ID ADS19462 standard; DNA; 708 BP.
XX
AC ADS19462;
XX
DT 16-DEC-2004 (first entry)
XX
DE Coding sequence DNA of the human CD8 alpha chain mRNA.

XX gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH 1..708
FT /*tag= a
FT /product= "CD8 alpha chain protein"

XX WO2004083404-A2.

XX 30-SEP-2004.

XX 19-MAR-2004; 2004WO-US008567.

XX 19-MAR-2003; 2003US-0456378P.

XX (ISOG-) ISOGENIS INC.

XX Qi Y, Zhang X, Konigsberg PJ;

XX WPI; 2004-691049/67.
XX P-FSDB; ADS19436.

XX New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain operably linked to a nucleic acid encoding a transmembrane polypeptide, useful for inhibiting cellular and humoral components of the host immune responses.

XX Disclosure; Fig 2a; 94pp; English.

XX This invention relates to novel gene therapy vectors with reduced immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8 alpha chain operably linked to nucleic acid encoding a transmembrane polypeptide and a second nucleic acid representing the therapeutic gene of interest (for example ornithine carbamoyl transferase or beta glucosidase), whereby transcriptional and translational control elements direct expression thereof. The present invention describes a method to reduce an immune response against antigens derived from a gene therapy delivery system i.e., improving the expression of a therapeutic transgene in a host and improving viral expression vectors with reduced immunogenicity. Accordingly, these compositions are useful for inhibiting both the cellular and humoral components of the host immune responses against expression vectors and target cells transfected with the vectors. As such, they exhibit immunosuppressive activity. This polynucleotide is the coding sequence DNA of the human CD8 alpha chain mRNA of the invention.

SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.97e-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS19462 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiAlaAlaArg 20
Db 1 ATGGCCTTACCAGTGCAGCGCTTGTCTCGCGCTGGCCTTGTCTCCAGCCCGCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGGTGTCCCGCTGGATCGGACCTGGAACTGGGGCGAGACATGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGTCTCCAAACCCGAGCTCGGCTGTCTGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGCTGGACACCCAGCGTTCGGGCAAGAGTTGGGGGACACCTTCTCTCTC 300
Qy 101 ThrLeuSerAspPheArgArgGluAsnGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGTCTCGGCCCTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTTCAGCCACTTGTGCGCGTCTTCTCTGCCAGCGAAGCCACCGACG 420
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTTCGACGCCCTGTCTCTCTGCGC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGCGTCCGCGCCAGCGCGGGGCGCAGTGCACACGAGGGGCTGGACTTCGCC 540
Qy 181 CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCCCTTGGCCGGACTTGTGGGGTCTTCTCTCTGTCACTG 600
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCACCCCTTTACTGCAACACAGGAAACGAAAGACGTGTTTGCATATGTCCTCCGCGCT 660
Qy 221 ValValIysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 661 GTGGTCAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 705

RESULT 5

ADV42461
ID ADV42461 standard; cDNA; 708 BP.
XX
AC ADV42461;

XX DT 10-MAR-2005 (first entry)

XX Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 89.

XX microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.

no

XX OS Homo sapiens.
XX PN WO2004108899-A2.
XX PD 16-DEC-2004.
XX PF 04-JUN-2004; 2004WO-US017686.
XX PR 04-JUN-2003; 2003US-0475915P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Nicholson A, Vernon SD;
XX DR WPI; 2005-031682/03.
XX PT New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX PS Claim 1; SEQ ID NO 89; 254pp; English.
XX CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specification mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,976-93 Length: 708
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0

US-10-804-763-1 (1-235) x ADV42461 (1-708)

Oy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTTACCAAGTACCGCTTGTCTCTCCGCTGGCTTCTCTCTCCACGCCCGCAGG 60
Oy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCGTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 120
Oy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTCTGCTGTCACCCGACGTCGGGTGCTCTGCTCTCTCCAGCGC 180
Oy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 181 CG 240
Oy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTCTCGGCGCAAGAGTTGGGGGACACCTTCGTCCTC 300
Oy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCGGAGAACGAGGGCTACTATTTCTGCTCGCGCTCGAGCAAC 360
Oy 121 SerileMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTCAGCCACTTCGTGCGCGGTCTTCCTGCCAGCGAAGCCACCCAGCAG 420

Oy 141 ProAlaProArgProProThrProAlaProThrThrAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGGTGCGAGCCCTGTCCCTGCCG 480
Oy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGGGTGCCG 540
Oy 181 CysAspIleTyTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGCGCGCTTGGCGGGAGCTTGTGGGGTCTCTCTCTGTCTG 600
Oy 201 ValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 601 GTTATCATCCCTTTACTGCAACCCACAGAACCGAGACGTTGTTGCAAAATGTCGCCG 660
Oy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
Db 661 GTGGTCAATCGGGAGACAGCCCGAGCTTTCGGCGAGATACGTC 705

RESULT 6
AEF68357
ID AEF68357 standard; cDNA; 708 BP.
XX AC AEF68357;
XX DT 06-APR-2006 (first entry)
XX DE Human CD8 alpha chain cDNA.
XX KW immune inhibition; CD8; spinal cord injury; neuroprotective; vulnary;
KW autoimmune disease; immunosuppressive; immune disorder; diabetes;
KW antidiabetic; endocrine disease; gastrointestinal disease;
KW metabolic disorder; uveitis; antiinflammatory; ophthalmological;
KW inflammation; cirrhosis; hepatotropic; gastrointestinal disease;
KW neurodegenerative disease; neuroprotective; neurological disease;
KW osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease;
KW obesity; anorectic; nutritional disorder; ss; gene.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT 1..708
XX FT /*tag= b
XX FT /product= "CD8 alpha chain"
XX FT /transl_except= (pos:67..69,aa:Gly)
XX FT /transl_except= (pos:130..132,aa:Gly)
XX FT /transl_except= (pos:175..177,aa:Gly)
XX FT /transl_except= (pos:223..225,aa:Gly)
XX FT /transl_except= (pos:259..261,aa:Gly)
XX FT /transl_except= (pos:463..465,aa:Gly)
XX FT sig_peptide 1..63
XX FT /*tag= a
XX FT mat_peptide 64..705
XX FT /*tag= c
XX FT /product= "Mature CD8 alpha chain"
XX PN WO2006012416-A2.
XX PD 02-FEB-2006.
XX PF 20-JUL-2005; 2005WO-US025878.
XX PR 20-JUL-2004; 2004US-0589707P.
XX PR 29-SEP-2004; 2004US-0614529P.
XX PA (ISOG-) ISOGENIS INC.
XX PI Qi Y, Staerz UD;
XX DR WPI; 2006-125925/13.
XX DR P-PSDB; AEF68356.

late
two

PT New composition comprising CD8 polypeptide and autoantigen protein,
 PT useful for preventing or treating autoimmune disease, diabetes,
 PT neurodegenerative diseases, osteoarthritis.

XX Disclosure; Fig 1A; 85pp; English.

CC The invention relates to a therapeutic composition for inhibiting an
 CC autoreactive T cell response, comprising an expression vector encoding a
 CC CD8 polypeptide and an autoantigen protein or its fragment, or at least
 CC one epitope of an autoantigen associated with the autoreactive T cell
 CC response. Also described are: (1) a polynucleotide comprising a first
 CC nucleic acid sequence encoding a CD8 polypeptide, a second nucleic acid
 CC sequence encoding at least one epitope of an autoantigen associated with
 CC an autoreactive T cell response, and control sequences operably linked
 CC with the first and second nucleic acids for expression in a target cell;
 CC (2) a method for inhibiting an autoimmune response to a target antigen;
 CC and (3) a method of preventing the development of or for treating an
 CC autoimmune disease in a host. The composition and methods are useful for
 CC inhibiting an autoimmune response to a target antigen, and for preventing
 CC the development of or for treating autoimmune disease, diabetes, uveitis,
 CC cirrhosis, neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Huntington's disease, or Parkinson's disease), osteoarthritis, obesity,
 CC or spinal cord injury. The present sequence represents human CD8 alpha
 CC chain cDNA.

XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6, 97e-93 Length: 708
 Score: 1247.00 Matches: 235
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 15 Gaps: 0

US-10-804-763-1 (1-235) x AEF68357 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
 Db 1 ATGGCTTACCAAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCACGCCGCCAGG 60
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
 Db 61 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGACCTGGAACTCGGCGAGACAGTGGAG 120
 Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGAGCTCGGGCTGCTGTGGCTCTTCCAGCG 180
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
 Db 181 CGCGCGCGCGCGCGCGCGTCCACCTTCTCTATACCTCTCCAAACCAAGCCCAAGCG 240
 Qy 81 AlaGluGlyLeuAspThrClnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 241 GCCGAGGGCGTGGACACCGCGGTCTCGGCAAGAGTGGGGACACCTTCTGCTCTC 300
 Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 301 ACCCTGACGCGACTTCGCGCGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 361 TCCATCATGTACTTCAGCCACTTCGTGGCGGTCTTCTGCCAGCGAAGCCACCAACGAG 420
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 421 CCAGCGCGCGGACCAACCAACCGCGGCCACCATCGCGTGGCAGCCCTGTCTCTGCGC 480
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
 Db 481 CCAGAGCGGTGCGCGCGCGCGCGCGCGCGAGTGCACGAGGGGGTGGACTTCGCC 540

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
 Db 541 TGTGATATCATCATCTGGCGCCCTTGGCGGGACTTGTGGGGTCCCTCTCTGTCTGCTG 600
 Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
 Db 601 GTTATCACCTTTACTGCAACCCAGGACCGAAGACGTGTTTGCATAATGTCCCGGCGCT 660
 Qy 221 ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 235
 Db 661 GTGGTCAATCGGAGACAAGCCAGCGCTTTCGGCGGAGATACGTC 705

RESULT 7

AAQ57986

ID AAQ57986 standard; DNA; 1060 BP.

XX AC AAQ57986;

XX DT 25-MAR-2003 (revised)

XX DT 20-AUG-1994 (first entry)

XX DE Genomic sequence of human CD8.

XX KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;

XX OS fusion protein; CD8; fusion protein; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 66..773

XX FT /*tag= a

XX PN EP585943-A2.

XX PD 09-MAR-1994.

XX PF 03-SEP-1993; 93EP-00114153.

XX PR 04-SEP-1992; 92US-00940605.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Aruffo A, Hollenbaugh D, Ledbetter JA;

XX DR WPI; 1994-076264/10.

XX DR P-PSDB; AARS59550.

XX PT New nucleic acid encoding human gp39 T cell antigen - which is a ligand
 for the CD40 receptor, causing proliferation and differentiation of B
 cells and some cancer cells.

XX PS Disclosure; Fig 9; 39pp; English.

XX CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in
 CC AAQ57984 and AAR49548 respectively and contd. in plasmid CD8-hgp39,
 CC deposited with the ATCC as E. coli, CDM8 MC1061/p3-hgp39 and assigned
 CC accession No. 69050. The human T cell antigen gp39 is a ligand for the
 CC CD40 receptor. Soluble gp39 may be produced using the expression vector
 CC CD8-gp39. Chimeric genes may be constructed by fusing sequences encoding
 CC the extracellular domains of gp39 and CD8, pref. murine or human CD8
 CC protein, plasmid p3-shgp39 encoding the fusion protein of the
 CC extracellular domains from gp39 and CD8 is deposited in E.coli as ATCC
 CC 69049. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,14e-92 Length: 1060
 Score: 1247.00 Matches: 235
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0

Handwritten note:
 * C: in human *
 (with a star symbol)

Db 606 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTTGGGGGCTTCTCTGTCACTG 665
Qy 201 ValTleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTGCAATGTCCCGGCT 725

Qy 221 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAATCGGAGACAGCCAGCTTTTCGGCGAGATACGTC 770

RESULT 9

AD131688
ID AD131688 standard; cDNA; 1060 BP.

XX AC AD131688;

XX DT 17-JUN-2004 (first entry)

XX DE Human cDNA #1014.

XX KW Human; Gene; ss; immunological response; immunopathological condition;
XX KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
XX KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX OS Homo sapiens.

XX XX US6607879-B1.

XX XX 19-AUG-2003.

XX PF 09-FEB-1998; 98US-00023655.

XX PR 09-FEB-1998; 98US-00023655.

XX XX (INCY-) INCYTE CORP.

XX PI Cocks BG, Stuart SG, Seilhamer JJ;

XX XX WPI; 2003-895307/82.

XX PT A composition comprising a plurality of cDNAs, useful for detecting
XX PT altered expression of genes in an immunological response or for
XX PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX PT or osteoarthritis.

XX PS Claim 1; SEQ ID NO 1014; 50pp; English.

XX CC The invention relates to a composition comprising a plurality of cDNAs
XX CC for detecting the altered expression of genes in an immunological
XX CC response. The invention also relates to a method of diagnosing or
XX CC monitoring the treatment of an immunopathological condition in a sample,
XX CC comprising obtaining nucleic acids from a sample, contacting the nucleic
XX CC acids of the sample with an array comprising the plurality of cDNAs under
XX CC conditions to form one or more hybridisation complexes, detecting the
XX CC hybridisation complexes and comparing the levels of the detected
XX CC hybridisation complexes with the level of hybridisation complexes
XX CC detected in a non-diseased sample, where an altered level of the detected
XX CC hybridisation complexes correlates with the presence of an
XX CC immunopathological condition. Also disclosed are an expression profile
XX CC comprising a microarray and a plurality of detectable complexes and a
XX CC method for identifying a plurality of polynucleotide probes. The cDNAs
XX CC are useful as hybridisable array elements in a microarray for monitoring
XX CC the expression of target polynucleotides. The microarray can be used in
XX CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
XX CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX CC identifying agents for the treatment of the diseases. The microarray may
XX CC also be used in drug discovery and development, toxicological and
XX CC carcinogenicity studies, forensics or pharmacogenomics. The composition
XX CC may also be used in purification of a subpopulation of mRNAs, cDNAs or

CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the USPSTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. NO.: 1.14e-92 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservativeness: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-804-763-1 (1-235) x ADI31688 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 66 ATGGCCTTACAGTGACCGCCTTGTCTCTGCCGTGGCTTGTCTCCAGCGCCGAGG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAACCTGGGCGGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGTCTCAACCCGACGTGGGCTGTCTGTCTCTTCCAGCGG 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGGGCGCGCGCGAGTCCACCTTCTCTCTATACCTTCCCAAAAACAGCCCAAGGGG 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCGAGGGGCTGGACACCCAGCGGTCTCTCGGGCAAGAGTTGGGGGACACCTTCTCTC 365

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 425

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTCAGCCACTTGTGCGCGGTCTCTCTCCAGCGAAGCCACACGAGG 485

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACCAACACCGGCGCCACCATCGGCTCGCAGCCCTGTCTCTCGCGC 545

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGGCGTCCCGGCCAGCGCGGGGCGGCGAGTGCACACAGAGGGGCTGACTTCGCGC 605

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTCTTCTCTGTCTG 665

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTGCAAAATGTCCCGGCGCT 725

Qy 221 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235

Db 726 GTGGTCAATCGGAGACAGCCAGCTTTTCGGCGGAGATACGTC 770

RESULT 10

AD583755

ID AD583755 standard; cDNA; 1060 BP.

XX AC AD583755;

XX DT 11-AUG-2005 (first entry)

XX XX

DE Human lymph node cDNA #1014.
 XX ss; gene; human; immunological response; blood cell; cancer;
 KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
 KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
 KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
 XX
 OS Homo sapiens.
 XX
 XX US2004077003-A1.
 XX
 XX 22-APR-2004.
 XX
 XX 14-AUG-2003; 2003US-00641643.
 XX
 XX 09-FEB-1998; 98US-00023655.
 XX
 XX (INCY-) INCYTE CORP.
 XX
 XX Cocks BG, Stuart SG, Seilhamer JJ;
 XX
 XX WPI; 2004-387937/36.
 XX
 XX New compositions having a number of first, second and third
 PT polynucleotide probes, useful in research and diagnostic applications in
 PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
 PT infections.
 XX
 XX Claim 15; SEQ ID NO 1014; 16pp; English.
 XX
 XX The invention relates to polynucleotides which are used as probes to
 CC detect genes differentially expressed in an immunological response,
 CC abundantly expressed in an immunological response and/or coding for a
 CC polypeptide known to regulate blood cell biology. The polynucleotides are
 CC useful in research and diagnostic applications particularly in cancer and
 CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
 CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
 CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
 CC present sequence represents a human lymph node cDNA used to detect blood
 CC cell and immunological response gene expression. Note: The present
 CC sequence does not appear in the printed specification but was obtained in
 CC electronic format from the USPTO web site
 CC (seqdata.uspto.gov/sequence.html?DocID=2004007003).
 XX
 XX Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 1.14e-92 Length: 1060
 Score: 1247.00 Matches: 235
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS83755 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 DB 66 ATGGGCTTACCAAGTACCGCCCTTGCTCCGCGCTGGCCCTGCTCCACGCGCGCAGG 125
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTriPAsnLeuGlyuThrValGlu 40
 DB 126 CCGAGCCAGTTCCGGGTGTCGGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 185
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTriPLeuPheGlnPro 60
 DB 186 CTGAAGTGCAGGTGCTGCTGCTCCAACCGACGTCGGGTGCTCGTGGCTCTTCCAGCGG 245
 QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB 246 CGCGGCG 305
 QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

DB 306 GCCGAGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCGTCTC 365
 QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrrTyrrPheCysSerAlaLeuSerAsn 120
 DB 366 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCGTCTGGCCCTTGAGCAAC 425
 QY 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 DB 426 TCCATCATGTACTTCAGCCACTTCGTGCGCGCTTCCTGCCAGGAGGCCACACGACG 485
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 DB 486 CCAGGCGCGCGACCAACACCGCGCCACCATCGCTCGCAGCCCTGTCCCTGCGC 545
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
 DB 546 CCAGAGGGCGTCCGCGCCAGCGGGGGCGGAGTGACACAGAGGGGGCTGGACTTCGCC 605
 QY 181 CysAspIleTyrrIleTriPAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
 DB 606 TGTGATATCTACATCTGGCGGCCCTTGCGCGGACTTGTGGGGTCTCTTCTGTCTACTG 665
 QY 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
 DB 666 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGG 725
 QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
 DB 726 GTGGTCAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 11
 ADF90782
 ID ADF90782 standard; DNA; 2123 BP.
 XX
 XX ADF90782;
 XX
 XX 26-FEB-2004 (first entry)
 XX
 XX Human hepatic-fibrosis disease marker SEQ ID 244.
 XX
 XX Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 KW hepatic carcinoma; human; ds.
 XX
 XX Homo sapiens.
 XX
 XX JP2003259877-A.
 XX
 XX 16-SEP-2003.
 XX
 XX 11-MAR-2002; 2002JP-00065013.
 XX
 XX 11-MAR-2002; 2002JP-00065013.
 XX
 XX (SUMU) SUMITOMO SEIYAKU KK.
 XX
 XX WPI; 2003-821598/77.
 XX
 XX Hepatic fibrosis disease markers comprising polynucleotides or
 PT antibodies, useful for improved diagnosis, screening and developing drugs
 PT to treat hepatitis, to control cirrhosis and carcinoma.
 XX
 XX Claim 1; SEQ ID NO 244; 313pp; Japanese.
 XX
 XX The present invention relates to hepatic-fibrosis disease markers
 CC (ADF90339-ADF90871) and related proteins (ADF90872-ADF90917). The
 CC sequences are useful for detecting and treating hepatic fibrosis caused
 CC by alcohol consumption, virus infection, etc., and the associated chronic
 CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
 CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
 CC precision), so more suitable treatments can be developed and given.
 XX
 XX Sequence 2123 BP; 508 A; 586 C; 528 G; 501 T; 0 U; 0 Other;
 SQ

Alignment Scores:
Pred. No.: 2,69e-92 Length: 2123
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x ADF90782 (1-2123)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 81 ATGGCCCTTACAGTGACCGCTTGTCTCGCTGGCTTGTCTCCAGCCGCGCAGG 140

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 141 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGGACCTGGAACTGGGCGACAGTGGAG 200

Qy 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 201 CTGAAGTCCAGGTGCTGCTCCAAACCCGACGTCGGGCTGCTGGCTCTCCAGCG 260

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyriLeuSerGlnAsnLysProIysAla 80
Db 261 CGCGCGCGCGCGCGCGCTTCTCTATACCTTCTCCAAACCAAGCCCAAGGCG 320

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGluValAspThrPheValLeu 100
Db 321 GCCGAGGGGCTGGACACCCAGCGTTCGCGGCAAGAGTTGGGGACACCTTGTCTCTC 380

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyriTyriPheCysSerAlaLeuSerAsn 120
Db 381 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCTCTGAGCAAC 440

Qy 121 SerIleMetTyriPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 441 TCCATCATGTACTTCAGCCACTTGTGCGCGTCTTCTGCGGCGAAGCCCAACGACG 500

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 501 CCAGCGCGCGGACACACACCGCGCGCCACCATCGCTCGCAGCCCTGTCTCTGCGC 560

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 561 CCAGAGGCGTTCGCGCGCAGCGCGCGCGCGCGAGTGCACAGCGGGGCTGGACTTCGCC 620

Qy 181 CysAspIleTyriLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 621 TGTGATATCTACATCTGGGCGCGCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTG 680

Qy 201 ValIleThrLeuTyriCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 681 GTTATCACCTTTACTGCAACACAGAACCGAAGACGTGTTGCAATGTCCCGGCT 740

Qy 221 ValValIysSerGlyAspLysProSerLeuSerAlaArgTyriVal 235
Db 741 GTGGTCAATCGGAGACAGACCCAGCTTTTCGCGGAGATACGTC 785

RESULT 12

ADP10406

ID ADP10406 standard; DNA; 2261 BP.

XX AC

XX ADP10406;

XX AC

XX DT 12-AUG-2004 (first entry)

XX DE

XX Reference mRNA sequences for marker probe #83.

XX DE

XX transplant rejection; immune system; rheumatoid arthritis; lupus;

XX KW

XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

XX XX

XX Homo sapiens.

XX WO2004042346-A2.
XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325899.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX Claim 80; SEQ ID NO 415; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
XX and monitoring of allograft rejection and other disorders.
XX Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,91e-92 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-10-804-763-1 (1-235) x ADP10406 (1-2261)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACAGTGACCGCTTGTCTCGCTGGCTTGTCTCCAGCCGCGCAGG 179

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGGACCTGGAACTGGGCGACAGTGGAG 239

Qy 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTCCAAACCCGACGTCGGGCTGCTGGCTCTTCCAGCG 299

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyriLeuSerGlnAsnLysProIysAla 80
Db 300 CGCGCGCGCGCGCGCGCTTCTCTATACCTTCTCCAAACCAAGCCCAAGGCG 359

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGluValAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGGTGGGGACACCTTGTCTCTC 419

Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyriTyriPheCysSerAlaLeuSerAsn 120
Db 120

Db 420 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGGCGGTCTTCTGCCAGGAGGCCACAGCAG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCCACCAACCGCGCGCCACCATCGCTGCGAGGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGCTGCGCGGACGCGCGGGGGCGAGTGCACACGAGGGGCTTGACTTCGCC 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCACTG 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCCTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCCGGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAGCCACGCCCTTTCGGCGAGATACGTC 824

RESULT 13

ADS92791

ID ADS92791 standard; cDNA; 2261 BP.

XX AC

XX AD

XX AC

XX AD

XX DT

XX DT

XX DE

XX XX

XX KW

XX KW

XX OS

XX OS

XX FH

XX FT

XX FT

XX FT

XX FT

XX PN

XX XX

XX PD

XX XX

XX PF

XX XX

XX PR

XX XX

XX PA

XX XX

XX PI

XX XX

XX DR

XX DR

XX XX

XX PT

XX PT

XX PT

XX PT

XX PS

XX PS

XX CC

XX CC

XX CC

XX CC

XX CC

CC chain, where the CD8 polypeptide is expressed by the target cell and
CC where the host immune response against the target cell is specifically
CC inhibited. The method of the invention is useful for specifically
CC inhibiting both cellular and humoral immune responses to alloantigens,
CC thus finding use in extending the survival of transplant recipients and
CC in treating graft-versus-host disease in transplant recipients. The
CC present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
CC -chain may be used in the method of the invention.
XX

SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,91e-92 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-1 (1-235) x ADS92791 (1-2261)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiAlaAlaArg 20
Db 120 ATGGCCTTACCAGTACCCGCTTGTCTCGCCGCTGGCTTGTCTCCAGCCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTGCGGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGCTGTCTCAACCGACGTCGGGCTGTCTGGTGTCTTCCAGCCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyValAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTCTCGGCGAAGAGTTGGGGGACACCTTCGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTCGGGCTTCTCTGCCAGCAAGCCACCGACG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCCACCAACACCGCGGCCACCATCGCTCGAGCCCTGTCTCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGGGCTGCGCGCGAGCGCGGGGCGCAGTGCAACAGGGGGCTGGACTTCGCC 659
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGGCCCTTGTGCCGGGACTTGTGGGGTCTCTCTCTGTCT 719
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCCTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCCGGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAGCCACGCCCTTTCGGCGAGATACGTC 824

RESULT 14

ADS19437

ID ADS19437 standard; DNA; 2261 BP.

XX

No

Specifically inhibiting host immune responses to alloantigens, useful for
e.g. treating graft-versus-host disease, comprises contacting a target
cell expressing the antigen with an expression vector encoding a CD8
polypeptide.

Disclosure; Fig 1; 98pp; English.

The specification describes a method for specifically inhibiting a host
immune response to target cell-specific antigens (e.g. alloantigens). The
method comprises contacting a target cell expressing the antigen with an
expression vector encoding a CD8 polypeptide comprising the CD8 alpha-

AC ADS19437;
 XX 16-DEC-2004 (first entry)
 XX DNA of the human CD8 alpha chain mRNA.
 XX gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
 XX humoral immune response; immunosuppressive.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 XX CDS 120..827
 FT /*tag= a
 FT /product= "CD8 alpha chain protein"
 XX WO2004083404-A2.
 XX 30-SEP-2004.
 XX 19-MAR-2004; 2004WO-US008567.
 XX 19-MAR-2003; 2003US-0456378P.
 XX (ISOG-) ISOGENIS INC.
 XX Qi Y, Zhang X, Konigaberg FV;
 XX WPI; 2004-691049/67.
 XX P-PSDB; ADS19436.
 XX New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
 XX operably linked to a nucleic acid encoding a transmembrane polypeptide,
 XX useful for inhibiting cellular and humoral components of the host immune
 XX responses.
 XX Disclosure; Fig 1; 94pp; English.
 XX This invention relates to novel gene therapy vectors with reduced
 XX immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
 XX alpha chain operably linked to nucleic acid encoding a transmembrane
 XX polypeptide and a second nucleic acid representing the therapeutic gene
 XX of interest (for example ornithine carbamoyl transferase or beta
 XX glucosidase), whereby transcriptional and translational control elements
 XX direct expression thereof. The present invention describes a method to
 XX reduce an immune response against antigens derived from a gene therapy
 XX delivery system i.e. improving the expression of a therapeutic transgene
 XX in a host and improving viral expression vectors with reduced
 XX immunogenicity. Accordingly, these compositions are useful for inhibiting
 XX both the cellular and humoral components of the host immune responses
 XX against expression vectors and target cells transfected with the vectors.
 XX As such, they exhibit immunosuppressive activity. This polynucleotide is
 XX the DNA sequence of the human CD8 alpha chain mRNA of the invention.
 XX SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,91e-92 Length: 2261
 Score: 1247.00 Matches: 235
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 13 Gaps: 0
 US-10-804-763-1 (1-235) x ADS19437 (1-2261)
 Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 Db 120 ATGGCTTTACAGTGACCGCTTGTCTCGCGTGGCTTGTCTCCACGCGCCAGG 179
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 180 CCGAGCCAGTTCGGGGTGTGGCCGTGGATCGGACCTGGACCTGGCGGACAGACAGTGGAG 239

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 240 CTGAAGTGCCAGGTGCTGTGTCCAAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGG 299
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 300 CGCGGCCCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACACGCCACGAGCG 359
 Qy 81 AlaGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 360 GCGGAGGGCTGGACACCCAGCGCTTCTCGGGCAAGAGTTGGGGGACACCTTGTCTCTC 419
 Qy 101 ThrLeuSerAspPheArgArgGluAsnGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 420 ACCCTGAGCGACTTCCGCGGAGAGACGAGGGCTACTATTCTCTCGGCCCTGAGCAAC 479
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
 Db 480 TCCATCATGTACTTTCAGCCACTTCTGCGCGGTCTTCTTCCGAGGAGGCCACACGAGG 539
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 540 CCAGCGCGCGGACCCACACACCGCGGCCACCATCGCTCGAGGCCCTGTCCCTGCGC 599
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
 Db 600 CCAGAGCGGTGCCGCGCAGCGCGGGGGCGGCGAGTGCACACGAGGGGCTGGACTTCGCC 659
 Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
 Db 660 TGTATATCATCATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACTG 719
 Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
 Db 720 GTTATCACCTTTACTGCAACCCACAGGAACCGAAGCGTGTTCGAAATGTCCCGGCGCT 779
 Qy 221 ValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
 Db 780 GTGTGCAATCGGAGACAAGCCAGCGCTTTCGGCGAGATACGTC 824
 RESULT 15
 ADM86779
 ID ADM86779 standard; DNA; 2261 BP.
 XX AC ADM86779;
 XX DT 07-APR-2005 (first entry)
 XX DE Human CD8 gene.
 XX KW protein interaction; fusion protein; ss; PCR; primer.
 XX OS Homo sapiens.
 XX FN WO2005007822-A2.
 XX PD 27-JAN-2005.
 XX PF 09-JUL-2004; 2004WO-US021887.
 XX PR 09-JUL-2003; 2003US-0485988P.
 XX PR 15-OCT-2003; 2003US-0511918P.
 XX PR 27-APR-2004; 2004US-0566113P.
 XX PA (SENT-) SENTIGEN BIOSCIENCES INC.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Lee KJ, Axel R, Strapps W, Barnea G;
 XX WPI; 2005-102091/11.
 XX PT Determining protein/protein interaction modulator comprises contacting

PT the compound to a cell transfected or transfected with G-protein coupled
XX receptor and arrestin.

Example 29; SEQ ID NO 99; 133pp; English.

CC The invention relates to a novel method for determining if a test-
CC compound modulates a specific protein/protein interaction or protein
CC interactions of interest. The method comprises contacting the compound to
CC a cell or samples of cells, each of which has been transfected or
CC transfected with a nucleic acid molecule. The invention further
CC comprises: a recombinant cell, transfected or transfected with any of the
CC nucleic acid molecules; an isolated nucleic acid molecule comprising, in
CC 5' to 3' order, any of the nucleotide sequences described; an expression
CC vector comprising the isolated nucleic acid molecule of above, operably
CC linked to a promoter; a fusion protein produced by expression of the
CC isolated nucleic acid molecule of above; and a test kit, useful for
CC determining if a test compound modulates a specific protein/protein
CC interaction of interest. The methods, nucleic acid molecules, and kit are
CC useful for determining if a test-compound modulates a specific
CC protein/protein interaction or protein interactions of interest. This
CC polynucleotide sequence represents the human CD8 gene used in the method
CC of the invention.

XX
SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 2,91e-92 | Length: | 2261 |
| Score: | 1247.00 | Matches: | 235 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
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US-10-804-763-1 (1-235) x ADW86779 (1-2261)

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| QY | 1 | MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg | 20 |
| DB | 120 | ATGGCCTTACCAGTACCGCCTTGCTCGCGCTGGCCTTGCTCTCCACGCCGACGG | 179 |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| DB | 180 | CGAGCCAGTTCGGGGTGTGGCGGTGGATCGGACCTGGAACTGGGGGAGACAGTGGAG | 239 |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| DB | 240 | CTGAAGTGCCAGGTGCTGTGTCCAAACCGACGTCGGCTGCTCGTGGCTCTTCCAGCGG | 299 |
| QY | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
| DB | 300 | CGCGCGCGCGCGCCAGTCCACCTTCCTTATACCTTCCCAAAACAAGCCCAAGGCG | 359 |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
| DB | 360 | GCCGAGGGGCTGGACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCTC | 419 |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
| DB | 420 | ACCTTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC | 479 |
| QY | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr | 140 |
| DB | 480 | TCCATCATGTACTTCAGGCACCTTCGTGGCGGTCTTCCTGCCAGCGAAAGCCACACGACG | 539 |
| QY | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| DB | 540 | CCAGCGCGCGACACCAACACCGCGCGCCACCATCGCGTGCAGCCCTGTCCCTGCGC | 599 |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla | 180 |
| DB | 600 | CCAGAGGGCTGCCGGCCAGCGGGGGGGGGCGAGTGCACACGAGGGGGCTGGACTTCGCC | 659 |
| QY | 181 | CysAspIleTyrIleThrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu | 200 |

| | | | |
|----|-----|---|-----|
| DB | 660 | TGTGATATCTACATCTGGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTTCTCTGTCACTG | 719 |
| QY | 201 | ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro | 220 |
| DB | 720 | GTTATCACCCCTTTACTGCAACCCACAGGAACCCGAAACGTTGTTGCAAAATGTCGCCGCT | 779 |
| QY | 221 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 235 |
| DB | 780 | GTGGTCAAAATCGGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC | 824 |

Search completed: May 30, 2006, 03:54:18
Job time : 910.723 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame plus p2n model

Run on: May 29, 2006, 11:19:03 ; Search time 252.367 Seconds
(without alignments)
2613.516 Million cell updates

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVKSGDKPSLSARYV 235

Scoring table: BLOSUM62

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| Ygapop | 10.0 | Ygapext | 0.5 |
| Fgapop | 6.0 | Fgapext | 7.0 |
| Delop | 6.0 | Delext | 7.0 |

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 28073332

Minimum DB seq length: 0

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Post-processing: Minimum Match

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HSPASIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEBEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELEAF=7

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Database : Issued Patents NA: *

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9: 9: /EMC_Celerra_SID33/ptodata/2/ina/RE_COMB.seq.*
10: 10: /EMC_Celerra_SID33/ptodata/2/ina/backfiles.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | SUMMARIES | | | | Description |
|---------------|-----------|-------|--------|----|--------------------|
| | Score | Match | Length | ID | |
| 1 | 1247 | 100.0 | 1060 | 2 | US-07-940-605A-11 |
| 2 | 1247 | 100.0 | 1060 | 2 | US-08-690-096-11 |
| 3 | 1247 | 100.0 | 1060 | 3 | US-09-023-655-1014 |
| 4 | 1238 | 99.3 | 2150 | 5 | US-10-131-831-9109 |
| 5 | 954 | 76.5 | 1131 | 3 | US-08-751-512-7 |
| 6 | 623 | 50.0 | 822 | 2 | US-08-403-853-11 |
| 7 | 526 | 42.2 | 803 | 3 | US-09-477-737-2 |
| 8 | 526 | 42.2 | 972 | 2 | US-07-940-605A-9 |

ALIGNMENTS

RESULT 1

US-07-940-605A-11
Sequence 11, Application US/07940605A
Patent No. 5540926
GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07940.605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090

TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-940-605A-11

Alignment Scores:
Pred. No.: 5.54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x US-07-940-605A-11 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACAGTGACCGCTTCTCTCGCGTGGCTTGTCTCCAGCGCCGAGG 125
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGTGCGCGTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCAGCGG 245
Qy 61 ArgGlyAlaAlaAsaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACAGCCCAAGCGG 305
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACACCGCGGTCTCGGGCAAGAGGTGGGGGACACCTTCGTCTC 365
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGACGAGCTTCCGCGGAGAGACGAGGCTACTATTCTGCTCGGCTTGAGCAAC 425
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 426 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTCGCAGCGAAGCCACACGAGG 485
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGGAGCTGCTGCTGCGG 545
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGGGGTGCGCGGCCAGCGCGGGCGCGAGTGCACACGAGGGGGTGCACCTTCGCC 605
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 606 TGTGATATCATCTCGCGGCGCTTGGCGGAGCTTGTGGGGTCTTCTCTGTCACTG 665
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTTGTTGCAAAATGTCCCGGCT 725
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAAAATCGGGAGACAAGCCCGCTTTCGGCGAGATACGTC 770

RESULT 2
US-08-690-096-11
Sequence 11, Application US/08690096
Patent No. 5945513

GENERAL INFORMATION:
APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,096
FILING DATE: 31-JUL-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,605
FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-184
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-690-096-11

Alignment Scores:
Pred. No.: 5.54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x US-08-690-096-11 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACAGTGACCGCTTCTCTCGCGTGGCTTGTCTCCAGCGCCGAGG 125
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCGGGTGCGCGTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTGTGGCTCTTTCAGCGG 245
Qy 61 ArgGlyAlaAlaAsaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACAGCCCAAGCGG 305
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACACCGGTCTCGGGCAAGAGGTGGGGGACACCTTCGTCTC 365
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

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Db 366 ACCCTGAGGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 425
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Db 606 TGTGATATCTACATCTGGGGCCCTTGGCGGGAGCTTGTGGGGTCCCTTCTCTGTCTG 665
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RESULT 3
US-09-023-655-1014
; Sequence 1014, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

CLONE: g179145
US-09-023-655-1014
Alignment Scores:
Pred. No.: 5,54e-106 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
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Db 126 CCGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACCTGGAACCTGGGCGGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTGCAGGTGCTGCTCCAACCCGACGCTCGGGCTGTCTGTGGGTCTTTCAGCGCG 245
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Db 606 TGTGATATCTACATCTGGGGCCCTTGGCGGGAGCTTGTGGGGTCTTCTCTGTCTGCTG 665
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Db 726 GTGGTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 770
RESULT 4
US-10-131-831-9109
; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121

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; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Alignment Scores:
Pred. No.: 1,01e-104 Length: 2150
Score: 1238.00 Matches: 234
Percent Similarity: 99.6% Conservative: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 99.3% Indels: 0
DB: 5 Gaps: 0

US-10-804-763-1 (1-235) x US-10-131-831-9109 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6 ATGGCTTTACAGTACGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCCAGG 65

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 66 CCGAGCCAGTTCGGGTGTGCGCGTGTGATCGGACCTGGACCTGGGCGAGACAGTGGAG 125

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTGGCTGTCTGTGGCTCTTCCAGCG 185

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGCGCGCGCGCGAGTCCACCTTCCTTCTATACCTCTCCCAAAACAGCCCAAGCG 245

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
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Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 306 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTGCTATTCTGCTCGGCCCTGAGCAAC 365

Qy 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 366 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTTCGCCAGCGAAGCCACCAAGCG 425

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 426 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTGGCAGCCCTGTCTCTGCGC 485

Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 486 CCAGAGGCGTGC CGCGCGCGCGCGGCGCAGTGCAACAGAGGGGCTGGACTTCGCC 545

Qy 181 CysAspIleTyrrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 546 TGTGATATCATCTGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTGCTG 605

Qy 201 ValIleThrLeuTyrrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 606 GTTATACCTTTACTGCAACACAGGAAACCGAAGCGTGTGTTGCAATGTCTCCGGCT 665

Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrrVal 235
Db 666 GTGGTCAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 710

US-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramer, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified FAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1128
US-08-751-512-7

Alignment Scores:
Pred. No.: 7,41e-79 Length: 1131
Score: 954.00 Matches: 181
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 76.5% Indels: 0
DB: 3 Gaps: 0

US-10-804-763-1 (1-235) x US-08-751-512-7 (1-1131)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTTACAGTACGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCCGCCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTGCGCGTGTGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTGGCTGTCTGTGGCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACAGCCCAAGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGCGGCTGGACACCCAGCGGTCTCGGCGAAGAGGTTGGGGGACACCTTCGCTCTC 300

RESULT 5
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QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCATCATGTACTTTCAGCCACTTCGTGCGCGTCTTCTGCGCAGGAGCCACCGACG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCCGCGACCAACACACCGCGGCCACCATCGCGTCGAGCCCTGTCCCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGAGTGCACACGAGGGGGCTGGACTTCGCC 540
QY 181 Cys 181
Db 541 TGT 543
RESULT 6
US-08-403-853-11
; Sequence 11, Application US/08403853
; Patent No. 584094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide

; LOCATION: 1..819
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 1..819
US-08-403-853-11
Alignment Scores:
Pred. No.: 1..89e-48 Length: 822
Score: 623.00 Matches: 124
Percent Similarity: 94.0% Conservative: 1
Best Local Similarity: 93.2% Mismatches: 2
Query Match: 50.0% Indels: 6
DB: 2 Gaps: 2
US-10-804-763-1 (1-235) x US-08-403-853-11 (1-822)
QY 9 LeuLeuProLeuAla-----LeuLeuLeuHisAlaAlaArgPro-----Ser 22
Db 10 CTATTGCGCTACGCGCAGCGCTGGATTGTTATTACTCGCTGCCCAACCGCATGGCCAGC 69
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 70 CAGTTCCGGGTGTCGCCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAGCTGAAG 129
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 130 TGCCAGGTGCTGCTGTCCAAACCGGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCGCGGC 189
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 190 GCCGCGCGCAGTCCACACCTTCCTCTATACCTCTCCCAAAACAAGCCCAAGCGCGCGAG 249
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 250 GGGCTGGACACCCAGCGGTTCTCGGCGAGAGGTTGGGGGACACCTTCTGCTCCCTCATC 309
QY 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db 310 AGCGACTTCCGCGCAGAGAACGAGGGCTACTATTCTGCTGGCCCTGAGCAACTCCATC 369
QY 123 MetTyrPheSerHisPheValProValPheLeuProAla 135
Db 370 ATGTACTTCAGCCACTTCGTGCGCGTCTTCTCTGCCAGCG 408
RESULT 7
US-09-477-737-2
; Sequence 2, Application US/09477737
; Patent No. 6544506
; GENERAL INFORMATION:
; APPLICANT: Reiser
; TITLE OF INVENTION: VETO CELLS EFFECTIVE IN PREVENTING GRAFT REJECTION AND DEVOID OF
; FILE OF INVENTION: VERSUS HOST POTENTIAL
; FILE REFERENCE: 00/20548
; CURRENT APPLICATION NUMBER: US/09/477,737
; CURRENT FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In ver. 2.1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-477-737-2
Alignment Scores:
Pred. No.: 1.7e-39 Length: 803
Score: 526.00 Matches: 124
Percent Similarity: 62.7% Conservative: 34
Best Local Similarity: 49.2% Mismatches: 72
Query Match: 42.2% Indels: 22
DB: 3 Gaps: 12
US-10-804-763-1 (1-235) x US-09-477-737-2 (1-803)

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Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 13 ATGGCCCTACCGTTGACCGCGTTCTGTCTGCTGAACCTGCTGCTGGGTGAGTCGATT 72
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 73 ATCTGGGGAGTGAGAGCTAAGCCACAGCAGCCCGAACTCCGAACTTTCCAAAGAA 132
Qy 31 ArgThrTrpAenLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 133 ATGACGCCGAACTTGGTCAGAGCTGACCTGCTGATGTAAGTG---TTGGGGTCCGTT 189
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 190 TCGCAAGGATGCTCTTGCTCTTCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 249
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 250 GTTGCTATATGCTTATCCACCAAGATAAGTGGGAGAGAGCTGAATTCGTGCG 309
Qy 88 Arg----PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 310 AAACCTGTTTTCTGCCATGAGGACACAGCAATAATAGTACGTTCTCACCTCGAACAGTTC 369
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 370 AGCAAGGAAACGAAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 429
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 430 AGTTCTGCTGCGCAGTCTTCAGAAAGTGAACCTACTACTACTACCAAGCAGTCTGCGCA 489
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 490 ACTCCCTCACCTGTGCACCTACCGGGACATCTCAGGCC-----CAGAGACCAGAAGAT 543
Qy 164 CysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
Db 544 TGTGCGCCCGT-----GGCTCAGTGAAGGGGACCGGATTTGGACTTCGCTGTGATATT 597
Qy 184 TyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
Db 598 TACATCTGGCACCTTGGCCGGAATCTGCTGGCCCTTCTGCTGCTTGTATCATCACT 657
Qy 204 LeuTyrCysAenHisArgAsnArgArgValCysLysCysProArgProValValLys 223
Db 658 CTCATCTGTACCAAGAGGCGAAAGCGTGTTCGAAATGTCCAGGCGCGCTAGTCAGA 717
Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 718 CAGGAAGCAAGCCAGACCTTCAGAGAAATTTGTG 753
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RESULT 8

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US-07-940-605A-9
; Sequence 9, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/940,605A
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; FILING DATE: 04-SEP-1992
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; CLASSIFICATION: 530
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; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Mistrock, S. Leslie
```

```
; REGISTRATION NUMBER: 18,872
```

```
; REFERENCE/DOCKET NUMBER: 5624-184
```

```
; TELEPHONE: 212 790-9090
```

```
; TELEFAX: 212 869-8864/9741
```

```
; TELEX: 66141 PENNIE
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; INFORMATION FOR SEQ ID NO: 9:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 972 base pairs
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; TYPE: nucleic acid
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; STRANDEDNESS: single
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```
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
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; US-07-940-605A-9
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Alignment Scores:
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Pred. No.: 2,22e-39 Length: 972
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Score: 526.00 Matches: 124
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Percent Similarity: 62.7% Conservative: 34
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Best Local Similarity: 49.2% Mismatches: 72
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Query Match: 42.2% Indels: 22
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DB: 2 Gaps: 12
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US-10-804-763-1 (1-235) x US-07-940-605A-9 (1-972)
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Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
Db 127 ATGGCCCTACCGTTGACCGCGTTCTGTCTGCTGAACCTGCTGCTGGGTGAGTCGATT 186
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 187 ATCTGGGGAGTGAGAGCTAAGCCACAGCAGCCCGAACTCCGAACTTTCCAAAGAA 246
Qy 31 ArgThrTrpAenLeuGlyThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 247 ATGACGCCGAACTTGGTCAGAGCTGACCTGCTGATGTAAGTG---TTGGGGTCCGTT 303
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 304 TCGCAAGGATGCTCTTGCTCTTCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 363
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 364 GTTGCTATATGCTTATCCACCAAGATAAGTGGGAGAGAGCTGAATTCGTGCG 423
Qy 88 Arg----PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 424 AAACCTGTTTTCTGCCATGAGGACACAGCAATAATAGTACGTTCTCACCTCGAACAGTTC 483
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 484 AGCAAGGAAACGAAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 544 AGTTCTGCTGCGCAGTCTTCAGAAAGTGAACCTACTACTACTACCAAGCAGTCTGCGCA 603
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 604 ACTCCCTCACCTGTGCACCTACCGGGACATCTCAGGCC-----CAGAGACCAGAAGAT 657
Qy 164 CysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
Db 658 TGTGCGCCCGT-----GGCTCAGTGAAGGGGACCGGATTTGGACTTCGCTGTGATATT 711
Qy 184 TyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
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Db 712 TACATCTGGGACACCTTGGCGGAATCTGCGTGCGCCCTTCTGCTGTCTGTGATCATCACT 771
|||||

Qy 204 LeuTyrcysAsnHisArgAsnArgAtqValCysLysCysProArgProValValLys 223
|||||

Db 772 CTCATCTGTACACAGGAGCCGAAAGCGTGTTCGAAATGTCACAGCCGCTAGTCAGA 831
|||||

Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
|||||

Db 832 CAGGAAGGCAAGCCAGACCTTCAGAGAAATTTGTG 867
|||||

RESULT 9

US-08-690-096-9

; Sequence 9, Application US/08690096

; Patent No. 5945513

; GENERAL INFORMATION:

; APPLICANT: ARUFFO, ALEJANDRO

; APPLICANT: HOLLENAUGH, DIANE

; APPLICANT: LEDBETTER, JEFFREY A.

; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,096

; FILING DATE: 31-JUL-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/940,605

; FILING DATE: 04-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 5624-184

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212 790-9090

; TELEFAX: 212 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 972 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-690-096-9

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 2,22e-39 | Length: | 972 |
| Score: | 526.00 | Matches: | 124 |
| Percent Similarity: | 62.7% | Conservative: | 34 |
| Best Local Similarity: | 49.2% | Mismatches: | 72 |
| Query Match: | 42.2% | Indels: | 22 |
| DB: | 2 | Gaps: | 12 |

US-10-804-763-1 (1-235) x US-08-690-096-9 (1-972)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuProLeuAlaLeu 14
|||||

Db 127 ATGGCTACACCTTGACCGCTTCTGCTGCTGAACCTGCTGCTGCTGGGTGAGTCGATT 186
|||||

Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
:::|||||

Alignment Scores:

Db 187 ATCTGGGGAGTGGAGAACTAAGCCACAGGACCCGAACTCCGAATCTTTTCAAAGAAA 246
|||||

Qy 31 ArgThrTyrAsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
|||||

Db 247 ATGGACGCCGAACCTTGGTCAGAAAGGTGGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 303
|||||

Qy 51 ThrSerGlyCysSerTyrLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
:::|||||

Db 304 TCGCAAGGATGCTCTTGGCTCTTCCAGAACTCCAGCTCCAAACTCCCCAGGCCACCTTC 363
|||||

Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
:::|||||

Db 364 GTTGTCTATATGCTTTCATCCCAACAAGATAAAGTGGACGAGAGAGCTGAATTCGTCG 423
|||||

Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
:::|||||

Db 424 AAATGTTTTCTGCCATGAGGACACAGTAAATAGTACGTTCTCACCTTGAACAAGTTC 483
|||||

Qy 106 ArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
:::|||||

Db 484 AGCAAGGAAACGAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543
|||||

Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
|||||

Db 544 AGTTCTGCTGCCAGTCTCTCAGAAAGTCAACTCTACTACTACCAAGCCAGCTGCTGCGA 603
|||||

Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
|||||

Db 604 ACTCCTCTACCTGTGCACCTTACCGGACATCTCAGCCC-----CAGAGCCAGAGAT 657
|||||

Qy 164 CysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
|||||

Db 658 TGTGGGCCCGT-----GGCTCAGTGAAGGGGACCGGATTGACTTCGCTGTGATATT 711
|||||

Qy 184 TyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
|||||

Db 712 TACATCTGGGACCCCTTGGCCGGAATCTGCTGGCCCTTCTGCTGTCTTGATCATCACT 771
|||||

Qy 204 LeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgProValValLys 223
|||||

Db 772 CTCATCTGTACACAGGAGCCGAAAGCGTGTTCGAAATGTCACAGCCGCTAGTCAGA 831
|||||

Qy 224 SerGlyAspLysProSerLeuSerAlaArgTyrVal 235
|||||

Db 832 CAGGAAGGCAAGCCAGACCTTCAGAGAAATTTGTG 867
|||||

RESULT 10

US-09-966-976A-8/c

; Sequence 8, Application US/09966976A

; Patent No. 6953688

; GENERAL INFORMATION:

; APPLICANT: Ferrick, David A.

; APPLICANT: Swift, Susan E.

; APPLICANT: Armstrong, Randall

; APPLICANT: Fox, Bryan

; TITLE OF INVENTION: Secretion and Compositions for Screening for Modulators and Ige Sy

; FILE OF INVENTION: Secretion and Switch Rearrangement

; CURRENT APPLICATION NUMBER: US/09/966,976A

; CURRENT FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US 09/076,624

; PRIOR FILING DATE: 1998-05-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 8345

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: synthetic

US-09-966-976A-8


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Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
   :::::::::::::::::::::
Db 556 ATCACCTGCAAGGCC--AGTCAGATGTGTATAATGCTGTGTGCTGTATCAACAGAAA 612
   :::::::::::::::::::::
Qy 61 ArgGlyAlaAlaLeuSerProThrPheLeuLeuValLeuSerGlnAsnLysProLysAla 80
   :::::::::::::::::::::
Db 613 CCAGA-----CAATCTCTAACTTCTGATTACTCGGCATCTCCCGGTACACTGGA 666
   :::::::::::::::::::::
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
   :::::::::::::::::::::
Db 667 GTC-----CCTTCTCGTTCACTGCGCAGTGGCTCTCGGCCCGGATTTCATTTC 714
   :::::::::::::::::::::
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTrpPheCysSer----- 116
   :::::::::::::::::::::
Db 715 ACCATCAGCAGTGTGCGAGCTGAAGACCTGCGCAGTTTATTCTGTGCAACAATTTTGGT 774
   :::::::::::::::::::::
Qy 117 ----- 120
   :::::::::::::::::::::
Db 775 ACTCCATTTCAGTTCCGGCTCGGGGACAAAATTGGAGATCAAAAGCTCTAGAGATCAGCAGAC 834
   :::::::::::::::::::::
Qy 121 SerLeuMetTrpPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
   :::::::::::::::::::::
Db 835 TCGGTGATGTTACTTTCAGTTCTGTGTCGAGTCTCTTTCAGAAAGTGAACCTCTACTACTACC 894
   :::::::::::::::::::::
Qy 141 ---ProAlaProArgProProThrProAla---ProThrIleAlaSerGlnProLeuSer 158
   :::::::::::::::::::::
Db 895 AAGCCAGTGTGCGGAACCTCCCTCACTGTGACCCCTACCGGACATCTCAGCCC----- 948
   :::::::::::::::::::::
Qy 159 LeuArgProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAsp 178
   :::::::::::::::::::::
Db 949 CAGAGACAGAGATTGTGCGCCCGT-----GCTCAGTGAAGGGACCGGATTGGAC 1002
   :::::::::::::::::::::
Qy 179 PheAlaCysAspIleTrpIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeu 198
   :::::::::::::::::::::
Db 1003 TTTCTAGAGGATCCCAAACTCTGCTACTTGTCTAGATGAATC-----CTCTTCATCTAC 1056
   :::::::::::::::::::::
Qy 199 SerLeuValIleThr---LeuTrpCysAsnHisArgAsnArgArgValCysLysCys 217
   :::::::::::::::::::::
Db 1057 GGAGTCAATCATCAGACCCCTGTACTGCTAGAGCAAAATTCAGCAGGATGTCAGA-GACTGC 1115
   :::::::::::::::::::::
Qy 218 ProArgProValValLysSerGlyAspLysProSerLeu 230
   :::::::::::::::::::::
Db 1116 TGCCAACT-----GCAGGACCCCAACACGCTCTA 1145
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RESULT 14

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US-08-751-359-21
; Sequence 21, Application US/08751359
; Patent No. 6143559
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,359
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
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; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB.504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-751-359-21

Alignment Scores:      0.035      Length:      5526
Pred. NO.:            135.00      Matches:      78
Score:                39.6%      Conservative: 32
Percent Similarity:    28.1%      Mismatches:  80
Best Local Similarity: 10.8%      Indels:      91
Query Match:          3          Gaps:        18
DB:

US-10-804-763-1 (1-235) x US-08-751-359-21 (1-5526)

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Db 604 GCCGTTTTCTCCCTCTCTCTCTCCCTCTCCAGGTCCCTGGTGCGAGCGGTGACT 663
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Qy 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
   :::::::::::::::::::::
Db 664 CAGCGGCTCTCGGTGTGAGCAAAACCG-----GGAGAAACCGTC 702
   :::::::::::::::::::::
Qy 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
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Db 703 AAGATCATCCTGTC-----TCCGGGATGAGGACTATATGGCTGG---TACCAG 747
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Qy 60 ProArgGlyAlaAlaLeuSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLys 79
   :::::::::::::::::::::
Db 748 CAGAGGACCTGCGCAGTGGCCCTGTCTACTGTATGTATGTACACACAGACCCCTCG 807
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Qy 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
   :::::::::::::::::::::
Db 808 GACATC-----CCTTACAGATTCTCCGGTTCCAAATCCGGCTCCACAGCCACA 855
   :::::::::::::::::::::
Qy 100 LeuThrLeuSerAspPheArgGluAsnGluGlyTrpPheCysSerAlaLeu--- 118
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Db 856 TTAACCATCACTGGGGTCCAGACCGCAGACAGGCTGTCTATTACTGTGGGAGTGC-AGA 914
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Qy 119 -----SerAsn----- 120
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Qy 129 ---ValProValPheLeu-----ProAlaLysProThrThrProAlaPro 143
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Db 1035 TCCTGCCCTGTGTGTCGACGCGCCGGTCTCTCTCGTTCCAGGCTGCACCCAGGTCCA 1094
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Qy 169 GlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIleTrpIle---TrpAla 187
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Db 1212 GAGGCCACCACTCAATTGCACTG-----TACATCAGCAGACA 1253
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Qy 188 ProLeuAlaGlyThrCysGlyValLeu-----LeuLeuSerLeuValIleThrLeuTr 205
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Db 1254 CAGTTCTCTT-ACATGTGTCCTCTGAGGAAAGAGTGGAGCTTCTTAAGCACCCTTAG- 1311
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US-08-907-146-21
; Sequence 21, Application US/08907146
; Patent No. 6316600
; GENERAL INFORMATION:
; APPLICANT: Michael, Nancy M
; APPLICANT: Accavitti, Marianne
; APPLICANT: Thompson, Craig B
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF CHICKEN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/907,146
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/751,359
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARSB:504
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-907-146-21

Alignment Scores:
Pred. No.: 0.035 Length: 5526
Score: 135.00 Matches: 78
Percent Similarity: 39.6% Conservative: 32
Best Local Similarity: 28.1% Mismatches: 80
Query Match: 10.8% Indels: 91
DB: 3 Gaps: 18

US-10-804-763-1 (1-235) x US-08-907-146-21 (1-5526)

QY 7 AlaLeuLeuProLeuAla-----LeuLeuHisAlaAla----- 19
Db 604 GCGGTTTCTCCCTCTCTCTCCCTCCAGGTTCCTGTCGAGCAGCGGTGACT 663
QY 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
Db 664 CAGCGGTCTCGGTGTGAGAAACCG-----GGAGAAACCGTC 702
QY 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
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QY 60 ProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLys 79
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QY 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
Db 808 GACATC-----CCTTCACGATTCTCGGTTCCAAATCCCGGCTCCACAGCCACA 855
QY 100 LeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeu--- 118
Db 856 TTAACCATCACTGGGGTCCAAAGCCGACGAGAGGCTGTCTATTACTGTGGAGTGC-AGA 914
QY 119 -----SerAsn----- 120
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QY 129 ---ValProValPheLeu-----ProAlaLysProThrThrProAlaPro 143
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QY 144 -----ArgProPro-----ThrProAlaProThrIle 152
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Db 1155 CTGGCAGCTCCTCATCTGCTCTCCCTCCACTGAGACCACCTGCC---CAGCCCATGCTG 1211
QY 169 GlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIleTyTrile---TrpAla 187
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Search completed: May 29, 2006, 12:46:40
Job time : 263.367 secs

GenCore version 5.1.8
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Run on: May 30, 2006, 04:14:31 ; Search time 1318.82 Seconds

(without alignments)

3284.288 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA.Main:

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|------------------------------------|
| 1 | 1247 | 100.0 | 708 | 9 | US-10-804-762-28 Sequence 28, Appl |

| | | | | | |
|----|--------|-------|------|----|--------------------|
| 2 | 1247 | 100.0 | 708 | 10 | US-10-804-763-28 |
| 3 | 1247 | 100.0 | 1060 | 6 | US-10-207-655-173 |
| 4 | 1247 | 100.0 | 1060 | 8 | US-10-641-643-1014 |
| 5 | 1247 | 100.0 | 2861 | 9 | US-10-804-762-2 |
| 6 | 1247 | 100.0 | 2861 | 10 | US-10-888-313A-99 |
| 7 | 1247 | 100.0 | 2861 | 10 | US-10-804-763-2 |
| 8 | 1167 | 93.6 | 692 | 7 | US-10-378-393-2 |
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| 10 | 1166.5 | 93.5 | 2411 | 7 | US-10-378-393-10 |
| 11 | 1162 | 93.2 | 689 | 7 | US-10-378-393-19 |
| 12 | 1162 | 93.2 | 690 | 7 | US-10-378-393-12 |
| 13 | 1162 | 93.2 | 1987 | 7 | US-10-378-393-17 |
| 14 | 1162 | 93.2 | 8858 | 7 | US-10-378-393-1 |
| 15 | 1149.5 | 92.2 | 2134 | 9 | US-10-723-860-5746 |
| 16 | 1094 | 87.7 | 708 | 9 | US-10-804-762-26 |
| 17 | 1094 | 87.7 | 708 | 10 | US-10-804-763-26 |
| 18 | 1008.5 | 80.9 | 597 | 9 | US-10-804-762-6 |
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| 21 | 1006.5 | 80.7 | 2150 | 10 | US-10-804-763-4 |
| 22 | 809 | 64.9 | 785 | 9 | US-10-804-762-22 |
| 23 | 809 | 64.9 | 785 | 10 | US-10-804-763-22 |
| 24 | 708.5 | 56.8 | 2001 | 9 | US-10-804-762-18 |
| 25 | 708.5 | 56.8 | 2001 | 10 | US-10-804-763-18 |
| 26 | 695.5 | 55.8 | 2179 | 9 | US-10-804-762-20 |
| 27 | 695.5 | 55.8 | 2179 | 10 | US-10-804-763-20 |
| 28 | 655 | 52.5 | 1330 | 9 | US-10-804-762-16 |
| 29 | 655 | 52.5 | 1330 | 10 | US-10-804-763-16 |
| 30 | 601 | 48.2 | 1229 | 9 | US-10-804-762-24 |
| 31 | 601 | 48.2 | 1229 | 10 | US-10-804-763-24 |
| 32 | 562.5 | 45.1 | 1010 | 9 | US-10-804-762-14 |
| 33 | 562.5 | 45.1 | 1010 | 10 | US-10-804-763-14 |
| 34 | 562.5 | 45.1 | 1010 | 16 | US-11-136-537-2941 |
| 35 | 526 | 42.2 | 803 | 3 | US-09-477-737-2 |
| 36 | 523 | 41.9 | 1452 | 9 | US-10-804-762-10 |
| 37 | 523 | 41.9 | 1452 | 10 | US-10-804-763-10 |
| 38 | 517 | 41.5 | 744 | 9 | US-10-804-762-12 |
| 39 | 517 | 41.5 | 744 | 10 | US-10-804-763-12 |
| 40 | 494 | 39.6 | 933 | 9 | US-10-804-762-8 |
| 41 | 494 | 39.6 | 933 | 9 | US-10-804-762-30 |
| 42 | 494 | 39.6 | 933 | 10 | US-10-804-763-8 |
| 43 | 494 | 39.6 | 933 | 10 | US-10-804-763-30 |
| 44 | 471.5 | 37.8 | 922 | 7 | US-10-311-455-2246 |
| 45 | 471.5 | 37.8 | 922 | 7 | US-10-240-485-186 |

ALIGNMENTS

RESULT 1

US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US2005004217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransjection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Alignment Scores: 3.17e-125 Length: 708
Pred. No.: 1247.00 Matches: 235

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Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-762-28 (1-708)

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Db 1 ATGGCCCTTACCAGTACCGGCTTCTCGCGCTGGCTTGTCTCCAGCCGCCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGGGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 300

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
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Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
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Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGCTCGCAGCCCTGTCCCTGCGC 480

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 481 CCAGAGGGCTGCCGCGCAGCGCGGGGGCGGACGAGTGCACACGAGGGGGCTGGACTTCGCC 540

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 541 TGTGATATCTACATCTGGGGCCCTTGGCGGACTTGTGGGGTCTTCTCTCTGTCACTG 600

Qy 201 VallieThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
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Qy 221 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
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RESULT 2
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; Sequence 28, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; PRIORITY FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-28
Alignment Scores: 3.17e-125 Length: 708
Pred. No.: 1247.00 Matches: 235
Score: 1247.00 Conservatives: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 100.0% Gaps: 0
DB: 10

US-10-804-763-1 (1-235) x US-10-804-763-28 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCCTTACCAGTACCGGCTTGTCTCGCGCTGGCTTGTCTCCAGCCGCCAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACCTGGGGGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 300

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Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
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Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
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Qy 201 VallieThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
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; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
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NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patent version 3.0
SEQ ID NO 173
LENGTH: 1060
TYPE: DNA
ORGANISM: Homo sapiens
US-10-207-655-173

Alignment Scores:
Pred. No.: 5,33e-125 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-1 (1-235) x US-10-207-655-173 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 66 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluValGlu 40
DB 126 CCGAGCCAGTTCGGGTGCGCGCTGGATCGACCTGGAACCTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTCCAGTGTCTGTCTCCACCGAGCTGGGCTGTCTGGCTCTTCCAGCGC 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 246 CGCGCGCGCGCGCGCGCTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGCTGGACACCGAGCGGTCTCGGCAAGAGGTGGGGGACACCTTCGCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
DB 366 ACCGTGAGGACCTTCGGCGGAGAGAACGAGGCTACTATTCTGTCTGGCCCTTGAGCAAC 425
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
DB 426 TCCATCATGTACTTCAGGCACCTTCGTGCGGTCTTCTGCCAGCAAGCCACACGACG 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCGAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCCGAGCCCTGTCTCTGCTG 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 546 CAGAGGGCGTCCGCGCAGCGCGGGGGGCGAGTGCACACAGGGGGCTGAGCTTCGCC 605
QY 181 CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
DB 606 TGTGATATCTACATCTGGCGCGCTTGGCGGACCTTGTGGGGTCTCTCTCTGCTGCTG 665
QY 201 ValIleThrLeuTyCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
DB 666 GTTATACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGAATAATGTCCCCG 725
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
DB 726 GTGTCAATCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 4

US-10-641-643-1014
Sequence 1014, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart

Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1014:
SEQUENCE CHARACTERISTICS:
LENGTH: 1060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: g179145
LIBRARY: GENBANK
SEQUENCE DESCRIPTION: SEQ ID NO: 1014 :
US-10-641-643-1014

No

Alignment Scores:
Pred. No.: 5,33e-125 Length: 1060
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-1 (1-235) x US-10-641-643-1014 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 66 ATGGGCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluValGlu 40
DB 126 CCGAGCCAGTTCGGGTGCGCGCTGGATCGACCTGGAACCTGGGCGAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTCCAGTGTCTGTCTCCACCGAGCTGGGCTGTCTGGCTCTTCCAGCGC 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
DB 246 CGCGCGCGCGCGCGCTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCG 305
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCCGAGGGGCTGGACACCGAGCGGTTCGGGCAAGAGGTGGGGGACACCTTCGCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120

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Db 366 ACCGTGAGCGACTTCCGCGGAGAACGAGGGCTACTATTCTGCTGGCCCTGAGCAAC 425
Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTACGCCACTTTCGTCCGGTCTTCTGCCAGCGAAGCCACACGACG 485
Qy 141 ProAlaProArgProProThrProAlaProThrThrLeuAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACACCGCGGCCACCACTCGCGTCCGACGCCCTGTCCCTGCGC 545
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyValAlaValHisThrArgGlyLeuAspPheAla 180
Db 546 CCAGAGCGTCCCGCGCAGCGCGGGGGCGGCGAGTGCACAGAGGGGCTGGACTTCGCC 605
Qy 181 CysAspileTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 606 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGCTACTG 665
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 666 GTTATCACCTTTACTGCAACACACAGGAAACGAAAGACGTGTTTGCATAATGTCCCGCGC 725
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 726 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 770

RESULT 5
US-10-804-762-2
; Sequence 2, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransjection
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-2

Alignment Scores:
Pred. No.: 1.41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x US-10-804-762-2 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACCAGTGACCGCCCTTGTCTCTCGCGCTGGCTTGTCTCCACGCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTTCGCGGTGATCGAATCGAATCGAATCGAATCGAATCGAATCGA 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTCTGCTGTCACCAACCGACGCTCGGGTGTCTGCTGCTCTTCCAGCGC 299
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 120 ATGGCCCTTACCAGTGACCGCCCTTGTCTCTCGCGCTGGCTTGTCTCCACGCGCCAGG 179
```

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Db 300 CGCGCGCGCGCGCGCGCTCCACCTTCTCTCTATACCTTCTCCAAACAAAGCCCAAGCGG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCTCCTC 419
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCGTGAGCGACTTCCGCGGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerileMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTACGCCACTTTCGTCCGGTCTTCTGCCAGCGAAGCCACACGACG 539
Qy 141 ProAlaProArgProProThrProAlaProThrThrLeuAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACACACCGCGGCCACCACTCGCGTCCGACGCCCTGTCCCTGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyValAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGCTGCCCGCGCAGCGCGGGGGCGGCGAGTGCACACAGGGGGCTGGACTTCGCC 659
Qy 181 CysAspileTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGCTACTG 719
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCTTTACTGCAACACACAGGAAACGAAAGACGTGTTTGCATAATGTCCCGCGC 779
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 824

RESULT 6
US-10-888-313A-99
; Sequence 99, Application US/10888313A
; Publication No. US20050100934A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Kevin
; APPLICANT: AXEL, Richard
; APPLICANT: STRAPPS, Walter
; APPLICANT: BARNEA, Gilad
; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction
; FILE REFERENCE: SENTI 203.2
; CURRENT APPLICATION NUMBER: US/10/888,313A
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/566,113
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60/511,918
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,968
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 101
; SEQ ID NO 99
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-888-313A-99

Alignment Scores:
Pred. No.: 1.41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-804-763-1 (1-235) x US-10-888-313A-99 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACCAGTGACCGCCCTTGTCTCTCGCGCTGGCTTGTCTCCACGCGCCAGG 179
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QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTGTCTCAACCCGAGCTCGGGTGTCTGTGGCTCTTCCAGCG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
DB 300 CGCGGGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACAAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCGAGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTGGGGGACACCTTCGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyLeuTyLeuSerGlnAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyLeuPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTGCGGAGGAGCCACAGCAG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGCGACGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 600 CCAGAGGGCTGCGCGGACGCGGCGGCGAGTGCACACAGAGGGGCTGGACTTCGCC 659
QY 181 CysAspIleTyLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
DB 660 TGTGATATCTACATCTGGCGGCTTGGCGGGACTTGTGGGGTCTCTCTCTGTACATG 719
QY 201 ValIleThrLeuTyLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 220
DB 720 GTTATCACCTTTACTTGCACCAACAGGACCGAGACGTGTTCGAAATGTCCTCCGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
DB 780 GTGGTCAATCGGAGACAAAGCCAGCCTTTCGGGAGATACGTC 824

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RESULT 7

```

US-10-804-763-2
; Sequence 2, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens

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Alignment Scores:

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Pred. No.: 1,41e-124 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

```

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DB: 10 Gaps: 0
US-10-804-763-1 (1-235) x US-10-804-763-2 (1-2261)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 120 ATGGGCTTTACCAAGTACCGCCTTGCTCTCGCGCTGGCCTTGCTGTCCACGCGCCAG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTGTCTCAACCCGAGCTCGGGTGTCTGTGGCTCTTCCAGCG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
DB 300 CGCGGGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACAAAGCCCAAGGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCGAGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTGGGGGACACCTTCGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyLeuTyLeuSerGlnAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 479
QY 121 SerIleMetTyLeuPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTGCGGAGGAGCCACAGCAG 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGCGACGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
DB 600 CCAGAGGGCTGCGCGGACGCGGCGGCGAGTGCACACAGAGGGGCTGGACTTCGCC 659
QY 181 CysAspIleTyLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
DB 660 TGTGATATCTACATCTGGCGGCTTGGCGGGACTTGTGGGGTCTCTCTCTGTACATG 719
QY 201 ValIleThrLeuTyLeuTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 220
DB 720 GTTATCACCTTTACTTGCACCAACAGGACCGAGACGTGTTCGAAATGTCCTCCGCT 779
QY 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyVal 235
DB 780 GTGGTCAATCGGAGACAAAGCCAGCCTTTCGGGAGATACGTC 824

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RESULT 8

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US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 692

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-2

Alignment Scores:
Pred. No.: 1,53e-116 Length: 692
Score: 1167.00 Matches: 219
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.6% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-2 (1-692)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 36 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCTTGTCTCTCCAGCGCCAGG 95

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCGCGGGTGTGCGCGTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 155

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGCCAACCGGACGTGGGCTGCTCGTGGCTCTTCCAGCGG 215

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 275

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCGCGGFTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 335

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGACGACTTCCGCGGAGAGACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 395

Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCGTCGCGGTCTTCTCGCCAGCGAAGCCCAACGACG 455

Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACCAACACCGCGGCCACCAATCGCGTGCAGCCCTGTCCCTGCGC 515

Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 516 CCAGGGCGGTGCCGCGCAGCGGGGGCGCGCAGTGCGACAGGGGGCTGGACTTCGCC 575

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 576 TGTGATATCTACATCTGGCGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 635

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArg 219
Db 636 GTTATCACCCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAATGTCCCCGG 692

RESULT 9
US-10-378-393-6
; Sequence 6, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
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; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-6

Alignment Scores:
Pred. No.: 5,95e-116 Length: 1995
Score: 1167.00 Matches: 219
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.6% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-6 (1-1995)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 53 ATGGCCCTTACCAGTGACCGCCTTGCTCTCGCGCTGGCTTGTCTCTCCAGCGCCAGG 112

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 113 CCGAGCCAGTTCGCGGGTGTGCGCGTGGATCGGACCTGGAAACCTGGGGCGAGACAGTGGAG 172

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 173 CTGAAGTCCAGGTGCTGCTGCCAACCGGACGTGGGCTGCTCGTGGCTCTTCCAGCGG 232

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 233 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 292

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 293 GCCGAGGGGCTGGACACCGCGGFTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 352

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 353 ACCCTGACGACTTCCGCGGAGAGACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 412

Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 413 TCCATCATGTACTTCAGCCACTTCGTCGCGGTCTTCTCGCCAGCGAAGCCCAACGACG 472

Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 473 CCAGCGCGCGACCAACACCGCGGCCACCAATCGCGTGCAGCCCTGTCCCTGCGC 532

Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 533 CCAGGGCGGTGCCGCGCAGCGGGGGCGCGCAGTGCGACAGGGGGCTGGACTTCGCC 592

Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
Db 593 TGTGATATCTACATCTGGCGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 652

Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArg 219
Db 653 GTTATCACCCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAATGTCCCCGG 709

RESULT 10
US-10-378-393-10
; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
```



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; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.:      8 6e-116      Length:      2411
Score:          1166.50      Matches:      222
Percent Similarity: 91.8%      Conservative: 2
Best Local Similarity: 91.0%      Mismatches: 5
Query Match:    93.5%      Indels:      15
DB:              7          Gaps:      1

US-10-804-763-1 (1-235) x US-10-378-393-10 (1-2411)

QY      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db      36  ATGGCCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTTCCACGCCGCGCAGG 95
QY      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      96  CCGAGCCAGTTCCGGGTGTTCGGCGTGGATCGGACCTGGGAACCTGGCGGAGACAGTGGAG 155
QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      156  CTGAAGTGCAGGTCTGTCTGCCAACCGAGCTGGGCTGTCTGTGGGTCTTCCAGCGG 215
QY      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuHisAlaAlaArg 80
Db      216  CGCGCGCGCGCGCGCAGTCCCACTTCTCTTATACCTTCTCCAAAACAGGCCCAAGGCG 275
QY      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      276  GCCAGGGGCGTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCTCTCTC 335
QY      101  ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db      336  ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGTCTGGGCCCTGAGCAAC 395
QY      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      396  TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGGAGGCCACACAGAGG 455
QY      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      456  CCAGCGCGCGGACCAACACCGCGCGGCGGCGAGTGCACACAGAGGGGCTGAGCTTCGCC 515
QY      161  ProGluAlaCysArgProAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db      516  CCAGAGGGCTGCGCGCCACGCGCGGGGCGGCGAGTGCACACAGAGGGGCTGAGCTTCGCC 575
QY      181  CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db      576  TGTGATATCTACATCTGGCGGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCTCAGT 635
QY      201  ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro----- 218
Db      636  GTTATCACCTTTTACTGTCAACACACAGAACCGAGCGGTGTTGCAATGTCCTCCCTCAG 695
QY      219  -----ArgProValValLysSerGly 225
Db      696  TCTACGATCGGAGACTGCTCGAGAAACGGAGCTGGTGGAGCCGCTGACACTAGCGGA 755

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QY      226  AspLysProSer 229
Db      756  GCGATGCCCAAC 767

RESULT 11
US-10-378-393-19
; Sequence 19, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-19

Alignment Scores:
Pred. No.:      5 3e-116      Length:      689
Score:          1162.00      Matches:      218
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    93.2%      Indels:      0
DB:              7          Gaps:      0

US-10-804-763-1 (1-235) x US-10-378-393-19 (1-689)

QY      1  MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db      36  ATGGCCTTACCAAGTACCGCTTGTCTCGCGCTGGCTTGTCTTCCACGCCGCGCAGG 95
QY      21  ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      96  CCGAGCCAGTTCCGGGTGTTCGGCGTGGATCGGACCTGGGAACCTGGCGGAGACAGTGGAG 155
QY      41  LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      156  CTGAAGTGCAGGTCTGTCTGCCAACCGAGCTGGGCTGTCTGTGGGTCTTCCAGCGG 215
QY      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuHisAlaAlaArg 80
Db      216  CGCGCGCGCGCGCGCAGTCCCACTTCTCTTATACCTTCTCCAAAACAGGCCCAAGGCG 275
QY      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      276  GCCAGGGGCGTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCTCTCTC 335
QY      101  ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db      336  ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGTCTGGGCCCTGAGCAAC 395
QY      121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      396  TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGGAGGCCACACAGAGG 455
QY      141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      456  CCAGCGCGCGGACCAACACCGCGCGGCGGCGAGTGCACACAGAGGGGCTGAGCTTCGCC 515
QY      161  ProGluAlaCysArgProAlaGlyAlaValHisThrArgGlyLeuAspPheAla 180

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Db 516 CCAGAGCGTCCCGCCAGCGCGGGGGCCAGTGCACACGAGGGGCTGGACTTCGCC 575
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 576 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTGTGGGGTCTCTCTCTGCTCACTG 635
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 636 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAATGTCCC 689

RESULT 12
US-10-378-393-12
; Sequence 12, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-12

Alignment Scores:
Pred. No.: 5,31e-116 Length: 690
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-12 (1-690)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 36 ATGGCTTTACAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCACG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCGGGTGTCCGCGCTGGATCGGACCTCGAACCTGGGCGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 215
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAACCAAGCCCAAGCG 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCCAGCGGTCTCTCGGCAAGAGTTGGGGGACACCTTCGTCCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 336 ACCGTGACGCACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 395
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCTGTCGGGTCTTCTTCCAGCGAAGCCCAACACGAG 455
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Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGGACACCAACACACCGCGCCACCATCGCGTCGACGCCCTGTCCCTGGCG 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 516 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGCATGTGCACACGAGGGGCTGGACTTCGCC 575
Qy 181 CysAspIleTyrIleTTPAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 576 TGTGATATCTACATCTGGCGCCCTTGGCCGGGACTGTGGGGTCTCTCTCTGCTCACTG 635
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 636 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAATGTCCC 689

RESULT 13
US-10-378-393-17
; Sequence 17, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-17

Alignment Scores:
Pred. No.: 2,07e-115 Length: 1987
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-17 (1-1987)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 37 ATGGCTTTACAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCACG 96
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 97 CCGAGCCAGTTCCGGGTGTCCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 156
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 157 CTGAAGTCCAGGTGCTGCTGTCCAAACCGGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 216
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 217 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAACCAAGCCCAAGCG 276
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 277 GCCGAGGGGCTGGACACCCAGCGGTCTCTCGGCAAGAGTTGGGGGACACCTTCGTCCTC 336
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
```

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Db 337 ACCTGAGGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 396
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 397 TCCATCATGTACTTCAGCCACTTCGTGCGGGCTTCCTGCCAGCGAAGCCACACGAG 456
QY 141 ProAlaProArProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 457 CCAGCGCCGCGACCAACACCGCGGCCACCATCGCGTCGAGCCCTGTCCCTGCGC 516
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 517 CCAGAGCGGTGCCGCGCACGCGCGGGCGCGAGTGCAACAGAGGGGGTGGACTTCGCC 576
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 577 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCT 636
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 637 GTTATCACCCCTTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCC 690

RESULT 14
US-10-378-393-1
; Sequence 1, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 8858
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-1

Alignment Scores:
Pred. No.: 1.41e-114 Length: 8858
Score: 1162.00 Matches: 218
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.2% Indels: 0
DB: 7 Gaps: 0

US-10-804-763-1 (1-235) x US-10-378-393-1 (1-8858)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6321 ATGGCCCTTACCAGTGACCGCCCTTGCTCTCGCGCTGGCCCTTCTGCTCCACGCCGCCAGG 6380
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 6381 CCGAGCCAGTTCGGGGTGTGCGCGTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 6440
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 6441 CTGAAGTGCAGGTGCTGTGTCACACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 6500
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 6501 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 6560
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QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 6561 GCGGAGGGGCTGGACACCACCGGTCTCTGGGCAAGAGGTTGGGGACACCTTCGTCCCTC 6620
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 6621 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 6680
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 6681 TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTCTGCCAGCGAAGCCACACGAG 6740
QY 141 ProAlaProArProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 6741 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCGAGCCCTGTCCCTGCGC 6800
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 6801 CCAGAGCGGTGCCGCGCACGCGCGGGCGCGAGTGCAACAGAGGGGGCTGGACTTCGCC 6860
QY 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 6861 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCT 6920
QY 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
Db 6921 GTTATCACCCCTTTACTGCAACACACAGAAACCGAAGACGTGTTTGCAAAATGTCCC 6974
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RESULT 15

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US-10-723-860-5746
; Sequence 5746, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
; METHODS FOR SCREENING FOR SOFT TISSUE SARCOMA MODULATORS
; FILE REFERENCE: 05882.0193 NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5746
; LENGTH: 2134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-5746
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Alignment Scores:
Pred. No.: 5.17e-114 Length: 2134
Score: 1149.50 Matches: 219
Percent Similarity: 93.2% Conservatives: 0
Best Local Similarity: 93.2% Mismatches: 1
Query Match: 92.2% Indels: 15
DB: 9 Gaps: 1
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US-10-804-763-1 (1-235) x US-10-723-860-5746 (1-2134)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACCAGCGACCGCCCTTGCTCTCGCGCTGGCCCTTCTGCTCCACGCCGCCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGGTGTGCGCGTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCAGGTGCTGTGTCACACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 299
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Qy      61  ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProIysAla  80
Db      300  CGCGCGCGCGCGCGAGTCCACCTTCCTCCTATACCTCTCCCAAAACAAGCCCAAGGCG  359

Qy      81  AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu  100
Db      360  GCCGAGGGGCTGGAC-----  374

Qy     101  ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn  120
Db     375  ACCCTGAGCGACTTCGCGGAGAGACGAGGGCTACTATTCTGCTGGCCCTGAGCAAC  434

Qy     121  SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr  140
Db     435  TCCATCATGTACTTCAGCCACTTCGTGCCGCTCTTCTGCCAGCGAAGCCACCACGACG  494

Qy     141  ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg  160
Db     495  CCAGCGCGCGACCAACACCGCGGCCCCACCATCGCGTGCAGCCCTGTCCCTGGCG  554

Qy     161  ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla  180
Db     555  CCAGAGGGGTGCGGCGCAGCGCGGGGGCGGAGTGCAACAGAGGGGCTGGACTTCGCC  614

Qy     181  CysAspIleTyrIleTrrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu  200
Db     615  TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTCTCTCTGTCACTG  674

Qy     201  ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro  220
Db     675  GTTATCACCCCTTACTTGCAACACAGGAACCGAAGACGTGTTGCAAAATGTCGCCGCGCT  734

Qy     221  ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal  235
Db     735  GTGGTCAAATCGGAGACAGCCCTTTCGGCGAGATACGTC  779
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Search completed: May 30, 2006, 07:32:02
Job time : 1323.82 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:15:35 ; Search time 23.3372 Seconds
(without alignments)
1705.079 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 NALPVTALLPLALLHAAR.....KCPRPVKSGDKPSLSARYV 235

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=200000000 -HOST=abs06p
-USER=US10804763 @CEN1.1.39 @runat_26052006_165105_14645 -NCPU=6 -ICPU=3
-NO_WRAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEVTIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Published Applications_NA_New.*

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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1247 | 100.0 | 2261 | 6 | US-10-511-937-415 |
| 2 | 139 | 11.1 | 1912 | 7 | US-11-293-697-1818 |
| 3 | 122 | 9.8 | 944 | 7 | US-11-293-697-1585 |
| 4 | 121.5 | 9.7 | 2081 | 7 | US-11-293-697-2348 |
| 5 | 120 | 9.6 | 720 | 7 | US-11-211-917-39 |
| 6 | 118 | 9.5 | 337 | 7 | US-11-211-917-35 |
| 7 | 117 | 9.4 | 707 | 6 | US-10-503-433B-19 |
| 8 | 115 | 9.2 | 720 | 7 | US-11-211-917-7 |
| 9 | 114 | 9.1 | 720 | 7 | US-11-211-917-15 |

| | | | | | | |
|----|-------|-----|------|---|--------------------|---------------------|
| 10 | 113 | 9.1 | 336 | 7 | US-11-211-917-3 | Sequence 3, Appl |
| 11 | 113 | 9.1 | 720 | 7 | US-11-211-917-55 | Sequence 55, Appl |
| 12 | 112 | 9.0 | 336 | 7 | US-11-211-917-11 | Sequence 11, Appl |
| 13 | 112 | 9.0 | 336 | 7 | US-11-211-917-93 | Sequence 93, Appl |
| 14 | 112 | 9.0 | 722 | 6 | US-10-503-433B-22 | Sequence 22, Appl |
| 15 | 112 | 9.0 | 796 | 6 | US-10-503-433B-24 | Sequence 24, Appl |
| 16 | 111.5 | 8.9 | 885 | 7 | US-11-154-103-33 | Sequence 33, Appl |
| 17 | 111 | 8.9 | 337 | 7 | US-11-211-917-51 | Sequence 51, Appl |
| 18 | 110.5 | 8.9 | 792 | 6 | US-10-503-433B-21 | Sequence 21, Appl |
| 19 | 110 | 8.8 | 337 | 7 | US-11-239-308-15 | Sequence 15, Appl |
| 20 | 110 | 8.8 | 704 | 6 | US-10-503-433B-15 | Sequence 15, Appl |
| 21 | 110 | 8.8 | 801 | 6 | US-10-503-433B-14 | Sequence 14, Appl |
| 22 | 109 | 8.7 | 764 | 6 | US-10-503-433B-11 | Sequence 11, Appl |
| 23 | 108 | 8.7 | 720 | 7 | US-11-211-917-31 | Sequence 31, Appl |
| 24 | 108 | 8.7 | 720 | 7 | US-11-211-917-63 | Sequence 63, Appl |
| 25 | 108 | 8.7 | 720 | 7 | US-11-211-917-79 | Sequence 79, Appl |
| 26 | 108 | 8.7 | 720 | 7 | US-11-211-917-101 | Sequence 101, Appl |
| 27 | 108 | 8.7 | 1954 | 7 | US-11-293-697-1648 | Sequence 1648, Appl |
| 28 | 107.5 | 8.6 | 2272 | 6 | US-10-196-749-345 | Sequence 345, Appl |
| 29 | 107 | 8.6 | 795 | 6 | US-10-503-433B-12 | Sequence 12, Appl |
| 30 | 106 | 8.5 | 336 | 7 | US-11-211-917-27 | Sequence 27, Appl |
| 31 | 106 | 8.5 | 337 | 7 | US-11-211-917-59 | Sequence 59, Appl |
| 32 | 106 | 8.5 | 337 | 7 | US-11-211-917-75 | Sequence 75, Appl |
| 33 | 106 | 8.5 | 608 | 7 | US-11-301-554-908 | Sequence 908, Appl |
| 34 | 106 | 8.5 | 706 | 6 | US-10-503-433B-17 | Sequence 17, Appl |
| 35 | 105.5 | 8.5 | 729 | 7 | US-11-154-103-20 | Sequence 20, Appl |
| 36 | 105.5 | 8.5 | 4027 | 7 | US-11-169-140-1 | Sequence 1, Appl |
| 37 | 105 | 8.4 | 330 | 7 | US-11-254-679-59 | Sequence 59, Appl |
| 38 | 105 | 8.4 | 431 | 1 | US-09-784-950-71 | Sequence 71, Appl |
| 39 | 105 | 8.4 | 431 | 1 | US-10-503-433B-16 | Sequence 16, Appl |
| 40 | 104 | 8.3 | 444 | 1 | US-09-784-950-63 | Sequence 63, Appl |
| 41 | 104 | 8.3 | 543 | 7 | US-11-301-554-970 | Sequence 970, Appl |
| 42 | 104 | 8.3 | 705 | 7 | US-11-211-917-23 | Sequence 23, Appl |
| 43 | 104 | 8.3 | 803 | 6 | US-10-503-433B-20 | Sequence 20, Appl |
| 44 | 104 | 8.3 | 2598 | 7 | US-11-312-958-31 | Sequence 31, Appl |
| 45 | 103 | 8.3 | 330 | 7 | US-11-254-679-43 | Sequence 43, Appl |

ALIGNMENTS

RESULT 1
US-10-511-937-415
; Sequence 415, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 415
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-415
Alignment Scores:

No - top - best - not - top - best

```
Pred. No.: 1 7e-97 Length: 2261
Score: 1247.00 Matches: 235
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-804-763-1 (1-235) x US-10-511-937-415 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACAGTACGCGCTTCTCTCGCGCTGGCTTGTCTCCAGCGCCGACG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCGCGGTGTCGCGCTGGATCGGACCTGGAACTTGGGCGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTTCCAACCCGACGCTGGGCTCTCGTGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaLeuSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCCCAAAACAAGCCCAAGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGTTGGGGGACACCTTCGTCCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGCGCGAGAACGAGGGCTACTATTTCGTCGCGCCCTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTAATTCAGCCACTTGTGCGCGTCTTCGCGCAGGAGCCACACGACG 539
Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGACCAACCAACCGCGCGCCACCATCGCGTGGCGCCCTGCTCGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyClyAlaValHisThrArgGlyLeuAspPheAla 180
Db 600 CCAGAGCGGTCCGCGCCAGCGCGCGGCGCGAGTGACACAGAGGGGCTGGACTTCGCC 659
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGACTTGTGGGTCTTCTCTGTCACTG 719
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 720 GTTATCACCCCTTACTGCAACACAGGAAACGAGACGTTGTCGCAATGTCCCGCGCT 779
Qy 221 ValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 780 GTGGTCAAAATCGGAGACCAAGCCAGCCCTTTCGCGGACATACGTC 824

RESULT 2
US-11-293-697-1818
; Sequence 1818, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1818
; LENGTH: 1912

US-10-804-763-1 (1-235) x US-11-293-697-1818 (1-1912)
Qy 10 LeuProLeuAlaLeuLeuLeuHisAlaAlaArg-----ProSerGlnPheArgValSer 27
Db 64 CTCCTCTCACTCCCTCTCTCACTCACTGTGCAGGACTTGGGCCCACTGTGATTGATTCAA 123
Qy 28 ProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeu 47
Db 124 CCACCTCTCAGCGTCTGGGACCCCGGCGAGACGCTCACCATCCTGTTCAGGAACACG 183
Qy 48 SerAsn--ProThrSerGlyCysSerTrpLeuPheGlnProArgGlyAlaAlaAlaSer 66
Db 184 TCCAAACATCGAAGAAAGCTGTTAATTTGTACAGCAAGTCCCGAGGGAGGCC----- 237
Qy 67 ProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGluGlyLeuAspThr 86
Db 238 CCCAAATCTCTCATATGATTCTATCGACGGCCCTCAGGGGTC-----CCT 285
Qy 87 GlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuLeuLeuLeuSerAspPheArg 106
Db 286 TCCCGATTCTCTGCTCCAAGTCTGGAACCTCAGCCTCCCTGGCCATCAGTGGACTCCGG 345
Qy 107 ArgGluAsnGluGlyTyrPheCysSerAlaLeuSer-----AsnSerIleMet 123
Db 346 TCTGACGATGAGGTTTTTATTTCTGCGGCATGGGACAGCGGCTGAATGGTCTTCTC 405
Qy 124 TyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAlaPro 143
Db 406 TTCGCGCGA-----GGGACCAAGCTGACCGTCTGAGTGAGTCC 444
Qy 144 ArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 445 TCTCCCGCTCTCTGCTCCCTCTTGTTCAA----- 477
Qy 164 CysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIle 183
Db 478 TGTGCTCTTCT-----CATCTTGTCTCTGAAT 489
Qy 184 TyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIleThr 203
Db 490 ----- 504
Qy 204 LeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 505 CTTTTT-----TCCAGATGCTCTCGCCT 528

RESULT 3
US-11-293-697-1585
; Sequence 1585, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1585
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; LENGTH: 944
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1585

Alignment Scores:
Pred. No.: 0.0343 Length: 944
Score: 122.00 Matches: 41
Percent Similarity: 46.3% Conservative: 15
Best Local Similarity: 33.9% Mismatches: 51
Query Match: 9.8% Indels: 14
DB: 7 Gaps: 6

US-10-804-763-1 (1-235) x US-11-293-697-1585 (1-944)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
||| ||||| ||| ||||| ||| :||| :||
Db 31 ATGAGGCTCCCT-----GCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGATCC 84
||| ||||| ||| ||||| ||| :||| :||
Qy 21 ProSerGlnPheArgVal-----SerProLeuAspArgThrTrpAsnLeuGlyGluThr 38
||| ||||| ||| ||||| ||| :||| :||
Db 85 AGTGGGAAATGTGATGACTCAGTCTCCACTCTCCCTCCCGTCACCCCTGGAGAGCCG 144
||| ||||| ||| ||||| ||| :||| :||
Qy 39 ValGluLeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCys 54
||| ||||| ||| ||||| ||| :||| :||
Db 145 GCCTCCATCTCTGCAGCTTAGTCAGAGCCCTCTGCATAGTAATGGATACAACATATGTG 204
||| ||||| ||| ||||| ||| :||| :||
Qy 55 SerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSer 74
||| ||||| ||| ||||| ||| :||| :||
Db 205 GATTGGTACCTGCAGAGCCAGGG-----CAGTCTCCACAGCTCTTGATCTTTTAACT 258
||| ||||| ||| ||||| ||| :||| :||
Qy 75 GlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnAtqPheSerGlyLysArgLeu 94
||| ||||| ||| ||||| ||| :||| :||
Db 259 TCTAATCGG-----GCCTCCGGGGTC---CCTGACAGGTTCAGTGGCAGTGGATCA 306
||| ||||| ||| ||||| ||| :||| :||
Qy 95 GlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPhe 114
||| ||||| ||| ||||| ||| :||| :||
Db 307 GGCACAGATTTTATCTAAAAATCAGTAGAGTGGAGGCTGAGGATGTTGGGGTTATTTC 366
||| ||||| ||| ||||| ||| :||| :||
Qy 115 Cys 115
|||
Db 367 TGC 369

RESULT 4
US-11-293-697-2348
; Sequence 2348, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2348
; LENGTH: 2081
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2348

Alignment Scores:
Pred. No.: 0.107 Length: 2081
Score: 121.50 Matches: 67
Percent Similarity: 32.2% Conservative: 30
Best Local Similarity: 22.3% Mismatches: 83
Query Match: 9.7% Indels: 121
DB: 7 Gaps: 17

US-10-804-763-1 (1-235) x US-11-293-697-2348 (1-2081)

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; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-39

Alignment Scores:
Pred. No.: 0.0356 Length: 720
Score: 120.00 Matches: 44
Percent Similarity: 44.1% Conservatives: 16
Best Local Similarity: 32.4% Mismatches: 60
Query Match: 9.6% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-1 (1-235) x US-11-211-917-39 (1-720)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGTCCTCCCTGCTCAGCTCTGGGGCTGTAATGCTCTGGGCTCTGGATCAGTGGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuLeuGluThrValGlu 40
Db 61 GATATTGATGATCACTCACTCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCCCTGCTCC 120
Qy 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGAGGCTTAGTCAGAGTGTCTGTATAGTAATGATGATCACTATTGGATTGG 180
Qy 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuLeuSerGlnAsn 76
Db 181 TACCTGCAGAGCCAGG-----CAGTCTCCACAGCTCTGTATTTGGTTCTTAAT 234
Qy 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGCTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
Qy 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys--S 116
Db 283 GATTTTACACTGAAATAATCAGCAGAGTGGAGGCTGAGGATGTGGGGTTTATTACTGCA 342
Qy 116 erAlaLeuSerAsnSerIleMetTyrPheSerHisPheValPro 130
Db 343 CAAGTTTACAACTCCATT-----CACTTTGGGCC 374

RESULT 6
US-11-211-917-35
; Sequence 35, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09

; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 19
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-4
US-10-503-433B-19

Alignment Scores:
Pred. No.: 0.0627 Length: 707
Score: 117.00 Matches: 29
Percent Similarity: 50.0% Conservatives: 17
Best Local Similarity: 31.5% Mismatches: 38
Query Match: 9.4% Indels: 8
DB: 6 Gaps: 3

; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-35

Alignment Scores:
Pred. No.: 0.0195 Length: 337
Score: 118.00 Matches: 39
Percent Similarity: 46.4% Conservatives: 12
Best Local Similarity: 35.5% Mismatches: 43
Query Match: 9.5% Indels: 16
DB: 7 Gaps: 5

US-10-804-763-1 (1-235) x US-11-211-917-35 (1-337)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCTCTGCGAGTCTAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGTGTCTGTATAGTAATGATGATCACTATTGGATTGGTACCTGCAGAGCCAGGG 138
Qy 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCTGTATCTATTGGTCTTAATCGG-----GCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCys--SerAlaLeuSerAsnSerI 122
Db 241 AGCAGATGGAGGCTGAGGATGTGGGTTTATTACTGATGCAAGTTTACAACTCCA 300
Qy 122 leMetTyrPheSerHisPheValPro 130
Db 301 TT-----CACTTTGGGCC 314

RESULT 7
US-10-503-433B-19
; Sequence 19, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 19
; LENGTH: 707
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-4
US-10-503-433B-19

Alignment Scores:
Pred. No.: 0.0627 Length: 707
Score: 117.00 Matches: 29
Percent Similarity: 50.0% Conservatives: 17
Best Local Similarity: 31.5% Mismatches: 38
Query Match: 9.4% Indels: 8
DB: 6 Gaps: 3
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US-10-804-763-1 (1-235) x US-10-503-433B-19 (1-707)
QY 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 439 GGGCAGAGGTCACCATCTCTGCTGCTGGAGGAGCTCCAAATCATCGGGCAGTCATGAT 498
QY 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db 499 GTACTGTGTATCAGCAGCTCCAGGAGCGGC-----CCCAAACTCTCATCTATGTT 552
QY 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 553 AACAAATTCGGCCCTCAGGGGTC-----CTGACCGATTCCTGGCTCCAAAG 600
QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTrp 113
Db 601 TCTGGCACCCTCAGCTCCCTGCCATCAGTGGGCTCCGTCGAGGATGAGCTGATAT 660
QY 114 PheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 661 TACTGTGGGCTCTTGATGACACATGTAAGTGGTAC 696
RESULT 8
US-11-211-917-7
; Sequence 7, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-7
Alignment Scores:
Pred. No.: 0.095 Length: 720
Score: 115.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.2% Indels: 10
DB: 7 Gaps: 4
US-10-804-763-1 (1-235) x US-11-211-917-7 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTAATGCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGAGTCACTCAGCTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGAGGTCTAGTCAGGCTCTGTATAGTATGATGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACTTGCAGAGCCAGGG-----CAGTCTCCACAGCTCTGATCTATTTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC-----CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGATTTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 339
RESULT 9
US-11-211-917-15
; Sequence 15, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-15
Alignment Scores:
Pred. No.: 0.116 Length: 720
Score: 114.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4
US-10-804-763-1 (1-235) x US-11-211-917-15 (1-720)
QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCCCTGGGCTGCTAATGCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGAGTCACTCAGCTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGAGGTCTAGTCAGGCTCTGTATAGTATGATGATACAACTTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACTTGCAGAGCCAGGG-----CAGTCTCCACAGCTCTGATCTATTTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC-----CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGATTTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 339
RESULT 10
US-11-211-917-3
; Sequence 3, Application US/11211917
```

```
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-3

Alignment Scores:
Pred. No.: 0.0518 Length: 336
Score: 113.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-3 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCACTCTCGAGGTCTAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCCTTGTATAGTAATAGTACAACTTTTGGATGTGTACTCGCAGAGCCAGGG 138
Qy 63 AlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGGTCTCTAATCGG-----GCCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 194 GGGTGC-----CCTGACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 241 AGCAGATTGGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 11
US-11-211-917-55
; Sequence 55, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 55
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-55

Alignment Scores:
Pred. No.: 0.141 Length: 720
Score: 113.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 9.1% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-55 (1-720)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHiaAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTGCTCAGCTCTCTGGGGCTGTATAGTCTCTGGGTCTCGGATCCAGTGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCTCCCTGCCCGTCACCCCTGGAGAGCGCGCTCC 120
Qy 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCTCGAGGCTAGTGCAGAGCCTCTCTGTATAGTAAATGGATATAACTATTGGATTGG 180
Qy 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsn 76
Db 181 TACCTGCAGAGCCAGGG-----CAGTCTCCACACTCTCTGATCTATTGGGTCTTAAT 234
Qy 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC---CCTGACAGGTTTCAGTGGCAGTGGTTTCAGGCAC 282
Qy 97 ThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGAGGCTGAGGATGTTGGGGTTTATTACTGC 339

RESULT 12
US-11-211-917-11
; Sequence 11, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-11

Alignment Scores:
Pred. No.: 0.063 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 9.0% Indels: 10
DB: 7 Gaps: 4
```

US-10-804-763-1 (1-235) x US-11-211-917-11 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
 Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCTGCAGGCTAGT 78
 Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
 Db 79 CAGAGCCTCTGTATAGTATGATGATACAACTTTTGGATGGTACTCGAGAGCCAGGG 138
 Qy 63 AlaAlaAaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAlaAaGlu 82
 Db 139 -----CAGTCTCCAGACTCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
 Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
 Db 184 GGGGTC---CCTGACAGGTTGATGGCAGTGGATCAGGCAGGCACAGATTTTACACTGAAATC 240
 Qy 103 SerAspPheArgGluAsnGluGlyTyrtPheCys 115
 Db 241 AGCAGAGTGAGCTGAGGATGTGGGGTTTATTACTGC 279

RESULT 13

US-11-211-917-93
 ; Sequence 93, Application US/11211917
 ; Publication No. US20060093600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADUE, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI
 ; APPLICANT: FENG, XIAO
 ; TITLE OF INVENTION: ANTIBODIES TO CD40
 ; FILE REFERENCE: ABX-PF/3 US
 ; CURRENT APPLICATION NUMBER: US/11/211,917
 ; CURRENT FILING DATE: 2005-08-25
 ; PRIOR APPLICATION NUMBER: US/10/292,088
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: 60/348,980
 ; PRIOR FILING DATE: 2001-11-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 93
 ; LENGTH: 336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-11-211-917-93

Alignment Scores:
 Pred. No.: 0.063 Length: 336
 Score: 112.00 Matches: 32
 Percent Similarity: 45.2% Conservative: 10
 Best Local Similarity: 34.4% Mismatches: 41
 Query Match: 9.0% Indels: 10
 DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-93 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
 Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCTGCAGGCTAGT 78
 Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
 Db 79 CAGAGCCTCTGTATAGTATGATGATACAACTTTTGGATGGTACTCGAGAGCCAGGG 138
 Qy 63 AlaAlaAaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAlaAaGlu 82
 Db 139 -----CAGTCTCCAGACTCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
 Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102

US-10-804-763-1 (1-235) x US-10-503-433B-22 (1-722)

Qy 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
 Db 438 GGGCAGAGGGTCACCATCTCTTGCACCTGGGAGCAGCTCCCAACATCGGGCAGGTCCAGAT 497
 Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaAaSerProThrPheLeuLeuTrpLeu 73
 Db 498 GTACACTGTATATCAGCAGCTCCAGAGAACGGCC-----CCAAACTCTCTATCTATGTT 551
 Qy 74 SerGlnAsnLysProLysAlaAaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
 Db 552 AACAAACATCGGCCCTCAGGGGTC-----CTGACCGATTTCTTGGCTCCAG 599
 Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrtPyr 113
 Db 600 TCTGGCACCCTCAGCCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGCTGATTAT 659

US-10-503-433B-24

Qy 114 PheCysSerAlaLeuSerAsnSerile 122
 Db 660 TACTGTGGCGCTTATGATGACAGTATT 686

RESULT 15

US-10-503-433B-24
 ; Sequence 24, Application US/10503433B
 ; Publication No. US20060099641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mats OHLIN
 ; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
 ; FILE REFERENCE: 12578/46301
 ; CURRENT APPLICATION NUMBER: US/10/503,433B
 ; CURRENT FILING DATE: 2004-08-02
 ; PRIOR APPLICATION NUMBER: PCT/EP03/00982
 ; PRIOR FILING DATE: 2003-01-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: SeqWin99
 ; SEQ ID NO 22
 ; LENGTH: 722
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: F8 mutated clone 2-20

US-10-503-433B-22

Alignment Scores:
 Pred. No.: 0.172 Length: 722
 Score: 112.00 Matches: 30
 Percent Similarity: 48.3% Conservative: 13
 Best Local Similarity: 33.7% Mismatches: 38
 Query Match: 9.0% Indels: 8
 DB: 6 Gaps: 3

US-10-804-763-1 (1-235) x US-11-211-917-11 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
 Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCTGCAGGCTAGT 78
 Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
 Db 79 CAGAGCCTCTGTATAGTATGATGATACAACTTTTGGATGGTACTCGAGAACGCCGG 138
 Qy 63 AlaAlaAaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAlaAaGlu 82
 Db 139 -----CAGTCTCCAGACTCTGATCTATTGGGTTCTAATCGG-----GCCTCC 183
 Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
 Db 184 GGGGTC---CCTGACAGGTTGATGGCAGTGGATCAGGCAGGCACAGATTTTACACTGAAATC 240
 Qy 103 SerAspPheArgGluAsnGluGlyTyrtPheCys 115
 Db 241 AGCAGAGTGAGCTGAGGATGTGGGGTTTATTACTGC 279

RESULT 13

US-11-211-917-93
 ; Sequence 93, Application US/11211917
 ; Publication No. US20060093600A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BEDIAN, VAHE
 ; APPLICANT: GLADUE, RONALD P.
 ; APPLICANT: CORVALAN, JOSE
 ; APPLICANT: JIA, XIAO-CHI
 ; APPLICANT: FENG, XIAO
 ; TITLE OF INVENTION: ANTIBODIES TO CD40
 ; FILE REFERENCE: ABX-PF/3 US
 ; CURRENT APPLICATION NUMBER: US/11/211,917
 ; CURRENT FILING DATE: 2005-08-25
 ; PRIOR APPLICATION NUMBER: US/10/292,088
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: 60/348,980
 ; PRIOR FILING DATE: 2001-11-09
 ; NUMBER OF SEQ ID NOS: 147
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 93
 ; LENGTH: 336
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-11-211-917-93

Alignment Scores:
 Pred. No.: 0.063 Length: 336
 Score: 112.00 Matches: 32
 Percent Similarity: 45.2% Conservative: 10
 Best Local Similarity: 34.4% Mismatches: 41
 Query Match: 9.0% Indels: 10
 DB: 7 Gaps: 4

US-10-804-763-1 (1-235) x US-11-211-917-93 (1-336)

Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
 Db 19 TCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCCATCTCTGCAGGCTAGT 78
 Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
 Db 79 CAGAGCCTCTGTATAGTATGATGATACAACTTTTGGATGGTACTCGAGAACGCCGG 138
 Qy 63 AlaAlaAaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAlaAaGlu 82
 Db 139 -----CAGTCTCCAGACTCTGATCTATTGGGTTCTAATCGG-----GCCTCC 183
 Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102

US-10-804-763-1 (1-235) x US-10-503-433B-22 (1-722)

Qy 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
 Db 438 GGGCAGAGGGTCACCATCTCTTGCACTGGGAGCAGCTCCCAACATCGGGCAGGTCCAGAT 497
 Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaAaSerProThrPheLeuLeuTrpLeu 73
 Db 498 GTACACTGTATATCAGCAGCTCCAGGAAACGGCC-----CCAAACTCTCTATCTATGTT 551
 Qy 74 SerGlnAsnLysProLysAlaAaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
 Db 552 AACAAACATCGGCCCTCAGGGGTC-----CTGACCGATTTCTTGGCTCCAG 599
 Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrtPyr 113
 Db 600 TCTGGCACCTCAGCCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGCTGATTAT 659

US-10-503-433B-24

Qy 114 PheCysSerAlaLeuSerAsnSerile 122
 Db 660 TACTGTGGCGCTTATGATGACAGTATT 686

RESULT 15

US-10-503-433B-24
 ; Sequence 24, Application US/10503433B
 ; Publication No. US20060099641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mats OHLIN
 ; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
 ; FILE REFERENCE: 12578/46301
 ; CURRENT APPLICATION NUMBER: US/10/503,433B
 ; CURRENT FILING DATE: 2004-08-02
 ; PRIOR APPLICATION NUMBER: PCT/EP03/00982
 ; PRIOR FILING DATE: 2003-01-30
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: SeqWin99
 ; SEQ ID NO 22
 ; LENGTH: 722
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: F8 mutated clone 2-20

US-10-503-433B-22

Alignment Scores:
 Pred. No.: 0.172 Length: 722
 Score: 112.00 Matches: 30
 Percent Similarity: 48.3% Conservative: 13
 Best Local Similarity: 33.7% Mismatches: 38
 Query Match: 9.0% Indels: 8
 DB: 6 Gaps: 3

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:13:46 ; Search time 5108.67 Seconds
(without alignments)
3858.452 Million cell updates/sec

Title: US-10-804-763-1

Perfect score: 1247

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 235

Scoring table:

BLASUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

-O=/abs/ABSSWEB spool/US10804763/runat_26052006_165054_14448/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US10804763 @CN 1 1 7986 @runat_26052006_165054_14448 -NCFU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database :

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_hic: *
7: gb_est2: *
8: gb_est7: *
9: gb_est8: *
10: gb_est9: *
11: gb_gss1: *
12: gb_gss2: *
13: gb_gss3: *
14: gb_gss4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1222 | 98.0 | 789 | 2 | BI819839 |
| 2 | 1207 | 96.8 | 804 | 2 | BI820808 |
| 3 | 1192 | 95.6 | 882 | 2 | BI820267 |
| 4 | 1176 | 94.3 | 780 | 2 | BI760947 |

ALIGNMENTS

| RESULT 1 | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5182049 5', | 789 bp | mRNA | linear | EST 04-OCT-2001 |
|------------|---|---|--------|------|--------|-----------------|
| LOCUS | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5182049 5', | 789 bp | mRNA | linear | EST 04-OCT-2001 |
| DEFINITION | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5182049 5', | 789 bp | mRNA | linear | EST 04-OCT-2001 |
| ACCESSION | BI819839 | 603041366F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5182049 5', | 789 bp | mRNA | linear | EST 04-OCT-2001 |
| VERSION | BI819839.1 | GI:15931389 | 789 bp | mRNA | linear | EST 04-OCT-2001 |
| KEYWORDS | EST. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| REFERENCE | 1 | (bases 1 to 789) | | | | |
| AUTHORS | NIH-MGC | http://mgc.nci.nih.gov/. | | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | | |
| JOURNAL | Unpublished (1999) | | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11454 row: d column: 18 High quality sequence stop: 788. | | | | | |

DA

DA931234 DA931234
CO646993 ILLUMIGEN
DN997301 TC111602
BI911195 603062918
BI835165 603089746
BI820031 603037212
DA946587 DA946587
CR619549 full-length
DR007174 TC101240
DB124972 DB124972
DA958887 DA958887
BI905877 603063005
DB110509 DB110509
DA91044 DA91044
DA974329 DA974329
DA826683 DA826683
DA952710 DA952710
DA371487 DA371487
DB121562 DB121562
BI760884 603043751
AL552456 AL552456
DA381496 DA381496
DB124907 DB124907
DA942852 DA942852
DB123733 DB123733
DA936371 DA936371
DA943842 DA943842
DB117237 DB117237
BX415859 BX415859
DB102835 DB102835
DB106910 DB106910
DB200083 DB200083
DA935416 DA935416
DA938336 DA938336
DA940758 DA940758
DB123661 DB123661
DB110036 DB110036
DA670538 DA670538
DA421985 DA421985

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FEATURES
    source      Location/Qualifiers
1..789
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5182049"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_115"
    /note="Organ: pooled brain, lung, testis; Vector:
    pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of 6 male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1,29e-96      Length:      789
Score:          1222.00      Matches:    234
Percent Similarity: 99.2%      Conservative: 0
Best Local Similarity: 99.2%      Mismatches: 1
Query Match:    98.0%      Indels:     1
DB:             2           Gaps:        0

US-10-804-763-1 (1-235) x B1819839 (1-789)

Qy      1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaAarg 20
Db      76 ATGGCCCTTACCAGTACCGCTTGTCTCGCGTGGCTTGTCTCCAGCGCCAGG 135

Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      136 CCGAGCCAGTTCGGGTGTCGCGCTGATCGGACCTGGAACCTGGCGAGACAGTGGAG 195

Qy      41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      196 CTGAAGTCCAGGTGCTCTCTCCAAACCGACGTCGGGCTGCTGTGCTCTTCCAGCG 255

Qy      61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProIysAla 80
Db      256 CGCGCGCGCGCGCGCGACCCAGCGGTTCGCGCAAGAGGTTGGGGGACACCTTGTCTCTC 315

Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      316 GCCGAGGGGGCTGGACACCCAGCGGTTCGCGCAAGAGGTTGGGGGACACCTTGTCTCTC 375

Qy      101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db      376 ACCCTGAGCGACTTCGCGCGAGAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAAC 435

Qy      121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      436 TCCATCATGTACTTTCAGCCACTTCGTGCGGTCCTTCTCGCCAGCAAGCCACACAGCAG 495

Qy      141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      496 CCAGCGCGCGACCAACACCGCGCCACCATCGGTCGCGACCCCTGTCTCTCTGCGC 555

Qy      161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThr-ArgGlyLeuAspPheAl 180
Db      556 CCAGAGGGCGTCCGCGCCAGCGCGGGGGCGCAGTGCACACAGAGGGGGCTGGAATTGCG 615

Qy      180 aCysAspIleTyTrpIleTAlaProLeuAlaGlyThrCysGlyValLeuLeuSerIle 200
Db      616 CTGTGATATCATCATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACT 675

Qy      200 uValIleThrLeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgPr 220
Db      676 GGTATATACCTTTACTCTCAACCAACAGGAAACGAGAGCGTGTTCGCAAAATGTCCCGGCC 735

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Qy      220 oValValIysSerGlyAspLysProSerLeuSerAlaAlaArgTrpVal 235
Db      736 TGTGTCAAATCGGAGACACAGCCAGCCTTTCGCGGAGATACGTC 781

RESULT 2
B1820808
LOCUS      B1820808      804 bp      mRNA      linear      EST 04-OCT-2001
DEFINITION      603034019P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
mRNA sequence.
ACCESSION      B1820808
VERSION      B1820808.1 GI:15932358
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11436 row: e column: 06
High quality sequence stop: 802.

FEATURES
    source      Location/Qualifiers
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    /organism="Homo sapiens"
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    /clone="IMAGE:5175149"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_115"
    /note="Organ: pooled brain, lung, testis; Vector:
    pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of 6 male brains, age range 23-27; 1
    male lung, age 27; and 1 male testis, age 69. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.8 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      2,73e-95      Length:      804
Score:          1207.00      Matches:    228
Percent Similarity: 97.9%      Conservative: 0
Best Local Similarity: 97.9%      Mismatches: 5
Query Match:    96.8%      Indels:     0
DB:             2           Gaps:        0

US-10-804-763-1 (1-235) x B1820808 (1-804)

Qy      3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSer 22
Db      7 TTACAGTACCGCCTTGTCTCGCGCTGGCTTGTCTCCAGCGCGAGCGGAGC 66

Qy      23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db      67 CAGTTCGGGGTGTGCGCGCTGATCGGACCTGGAACCTGGGGGAGACAGTGGAGCTGAAG 126

Qy      43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62

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Db      127  TGGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCCAGCGCGCGGC 186
QY      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAaSerProLysAlaAlaGlu 82
Db      187  GCGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAACAGCCCAAGCGCGCGAG 246
QY      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      247  GGGCTGGACACCGCGGTCTCTCGGCAAGAGGTTGGGGACACCTTCTGCTCTCACCTG 306
QY      103  SerAspPheArgArgGluAaSerGlyTyrTyrPheCysSerAlaLeuSerAaSerIle 122
Db      307  AGCGACTTCGCGGAGAACGAGGGCTACTATTCTGCTGGCCCTTGACCACTCCATC 366
QY      123  MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db      367  ATGTACTTCAGCCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACACGAGCGCGG 426
QY      143  ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db      427  CGCGGACCAACACCGCGGCCACCATCGGCTCGCAGCCCTGTCTCCCTGGCGCCAG 486
QY      163  AlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCys 182
Db      487  GCGTGGCGGCGCGCGCGGCGCGAGTGCACACAGAGGGGCTGGACTTCGCTGTGAT 546
QY      183  IleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeuValIle 202
Db      547  ATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGCTCTTCTCTCTGCTGCTATC 606
QY      203  ThrLeuTyrCysAaHisArgAaSerArgArgGValCysLysCysProArgProValVal 222
Db      607  ACCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCATAATGTCCCGGCGCT 666
QY      223  LysSerGlyAspLysProSerLeuSerAlaAaTyrVal 235
Db      667  AAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTC 705

RESULT 3
LOCUS   BI820267
DEFINITION BI820267 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5177885 5',
          mRNA sequence.
ACCESSION BI820267
VERSION   BI820267.1 GI:15931817
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 882)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgaabs-remail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
          Clone Distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Place: LLNL1443 row: 9 column: 06
          High quality sequence stop: 769.
          Location/Qualifiers
FEATURES             source
     1..882
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:5177885"
     /lab_host="DH10B"

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/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      6,37e-94      Length:      882
Score:          1192.00      Matches:    231
Percent Similarity: 98.3%      Conservative: 1
Best Local Similarity: 97.9%      Mismatches: 1
Query Match:    95.6%      Indels:     3
DB:              2          Gaps:         0

US-10-804-763-1 (1-235) x BI820267 (1-882)
QY      3  LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSer 22
Db      65  ATACCAGTGACCGCCTTGCTCTGCGCTGGCTTGTCTGCACGCCGCCAGCGCGAGC 124
QY      23  GlnPheArgValSerProLeuAspArgThrTyrPheLeuGlyValThrValGluLeuLys 42
Db      125  CAGTTCCCGGGTGTCCCGCTGGATCGGACCTCGGAACCTGGGCGAGACAGTGGAGCTGA 184
QY      43  CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrLeuPheGlnProArgGly 62
Db      185  TGCCAGGTGCTGCTCTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCCAGCGCGCGC 244
QY      63  AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAaSerProLysAlaAlaGlu 82
Db      245  GCGCGCGCGACGTCCTCTCTATACCTCTCCAAACCAAGCCCAAGCGCGCGAG 304
QY      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      305  GGGCTGGACACCCAGCGGTCTCGGCGAAGAGGTGGGGGACACCTTCTCTCTCACCTG 364
QY      103  SerAspPheArgArgGluAaSerGlyTyrTyrPheCysSerAlaLeuSerAaSerIle 122
Db      365  AGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAACTCCATC 424
QY      123  MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db      425  ATGTACTTCAGCCACTTGTGCGGCTTCTCTGCCAGCGAAGCCACACGCGCGAG 484
QY      143  ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db      485  CGCGACCAACCAACCGCGGCCACCATCGGCTCGCAGCCCTGTCTCTCGCGCCAGAG 544
QY      163  AlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAsp 182
Db      545  GGGTCCCGCGCAGCGCGGGCGCGAGTGCACACAGAGGGGCTGGACTTCCGCTGTGAT 604
QY      183  IleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeuValIle 202
Db      605  ATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGCTGCTGTTAT 664
QY      202  eThrLeuTyrCysAaHisArgAaSerArgArgValCysLysCysProArgProValVa 222
Db      665  CACCCTTTACTGCAACCAAGAGACGTGTTTGCATAATGTCCCGCGCTGTGGT 724
QY      222  LysSerGlyAspLys-ProSerLeuSerAlaAaTyrVal 235
Db      725  CAAATCGGGGAGACAATGCCCGAGCCCTTTCGGCGAGATACGTC 766

RESULT 4
BI760947

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LOCUS      BI760947              780 bp      mRNA      linear      EST 25-SEP-2001
DEFINITION 603043151F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
mRNA sequence.
ACCESSION  BI760947
VERSION     BI760947.1 GI:15752525
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
            Eukaryota; Metazoa; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 780)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLM11458 row: e column: 13
            High quality sequence start: 4
            High quality sequence stop: 756.
            Location/Qualifiers
                1..780
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5183604"
                /lab_host="DH10B"
                /clone_lib="NIH MGC 116"
                /note="Organ: pooled colon, kidney, stomach; Vector:
                pCMV-SPORT; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
                source anonymous pool of 3 colons, age 26 yo male, 49 yo
                female, 71 yo male colon; 46 yo male kidney, and pool of 2
                stomachs, 62 yo male and 70 yo female. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.4 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                023. Note: this is a NIH_MGC Library."

FEATURES             source
    source
    1..780
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:5183604"
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    /clone_lib="NIH MGC 116"
    /note="Organ: pooled colon, kidney, stomach; Vector:
    pCMV-SPORT; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of 3 colons, age 26 yo male, 49 yo
    female, 71 yo male colon; 46 yo male kidney, and pool of 2
    stomachs, 62 yo male and 70 yo female. Library is
    oligo-dT primed and directionally cloned (EcoRV site is
    destroyed upon cloning). Average insert size 1.4 kb,
    insert size range 1-3 kb. Library is normalized and
    enriched for full-length clones and was constructed by C.
    Gruber (Invitrogen). Research Genetics tracking code
    023. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      1.36e-92      Length:      780
Score:          1176.00      Matches:    233
Percent Similarity: 98.3%      Conservative: 0
Best Local Similarity: 98.3%      Mismatches: 1
Query Match:    94.3%      Indels:     4
DB:             2           Gaps:       0

US-10-804-763-1 (1-235) x BI760947 (1-780)

Qy      1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      67 ATGGCTTACCAGTGACCGCTTGCTCGCGCTGGCTTGCTCTCCAGCCGCCAGG 126

Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      127 CCGAGCAGTTCGCGGTGCGCGCTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 186

Qy      41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      187 CTGAAGTCCAGGTGCTGCTGTCTCAACCGCAGCTGGGCTGCTGCTGCTCTTCCAGCG 246

Qy      61 ArgGlyAlaAlaAsnProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAla 80
Db      247 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAACAAGCCCAAGCGG 306

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Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      307 GCCGAGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTC 366

Qy      101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db      367 ACCCTGAGCGCACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTTGAGCAAC 426

Qy      121 SerIleMetTyTrpPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      427 TCCATCATGTACTTCACCCACTTCGTCGCGGTCTTCCTGCCAGCAAGCCACCAAGAG 486

Qy      141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      487 CCAGCGCGGACCAACCAACACCGCGCCCAACCATCGCGTCGCGAGCCCTGTCCCTGGCG 546

Qy      161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db      547 CCAGAGCGGTGCCGCGCAGCGCGCGGCGCGCGACGTGCACACGAGGGGCTGACTTCGCC 606

Qy      181 CysAspIleTyTrpIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSer-Le 200
Db      607 TGTGATATCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTCTGCTCACTT 666

Qy      200 uValIleThr-LeuTyTrpCysAsnHisArgAsnArgArgValCysLysCysProArgP 220
Db      667 GGTATATCACCCCTTTACTGCAACCAACCAAGAACCGTGTGTTCGAA-TGTCCCGCGC 725

Qy      220 roValValLysSerGlyAspLysProSerLeu-SerAlaArgTyTr 234
Db      726 CTGTGGTCAAATCGGAGACAAGCCAGCCCTTTTCGGCGGAGATAC 770

RESULT 5
LOCUS      DA931234
DEFINITION DA931234 SPLEN1 Homo sapiens cDNA clone SPLN1000141 5', mRNA
sequence.
ACCESSION  DA931234
VERSION     DA931234.1 GI:82056788
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 838)
            Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
            Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
            Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Koshida, N.,
            Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
            Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
            Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
            Diversification of Transcriptional Modulation: Large-scale
            Identification and Characterization of Putative Alternative
            Promoters of Human Genes
            Genome Res. 16 (1), 55-65 (2006)
            16344560
            Contact: Takao Isogai
            FLJ Project (HRI Team)
            Helix Research Institute
            2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: flj-cdna@nifty.com
            NEDO human cDNA project (New Energy and Industrial Technology
            Developmental Organization, Japan); cDNA library construction:
            Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
            Research Association for Biotechnology (RAB) and Biotechnology
            Center, National Institute of Technology and Evaluation; 3'-end one
            pass sequencing: RAB.
            Location/Qualifiers
                1..838

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN1000141"
/tissue_type="spleen"
/clone_lib="SPLEN1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 6,15e-92 Length: 838
Score: 1169.00 Matches: 226
Percent Similarity: 98.3% Conservative: 1
Best Local Similarity: 97.8% Mismatches: 4
Query Match: 93.7% Indels: 1
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x DA931234 (1-838)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 89 ATGGCCCTTACAGTACCGCTTGTCTCCCGCTGGCTTGTCTCCACGCGCGCAGG 148
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 149 CCGAGCCAGTTCGGGTGTGGCGCTGGATCGGACCTGGAACCTGGCGGAGACAGTGGAG 208
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 209 CTGAAGTGCAGGTGTGTGTCCAAACCGACGTGGGTGTCTGTGGTCTTTCAGCGG 268
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 269 CGCGGCGCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCAAACCAAGCCCAAGCGG 328
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 329 GCGGAGGGGCTGGACACCGCGGTCTCGGCAAGAGGTGGGGACACCTTCTGTCTC 388
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 389 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTGGCCCTTGAGCAAC 448
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 449 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTCCAGCGAAGCCCAACGACG 508
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 509 CAGCGCGCGGACCAACACCGCGGCCACCATCGCGTCCGCGCCCTGTCTCTCGCGC 568
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 569 CCAGAGGGTGTCCGCGACCGCGGGGGCGGAGTGACACAGGGGGGTGGACTTCGCC 628
QY 181 CysAspIleTyIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 629 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTTCTCTGTCTG 688
QY 201 ValIleThrLeuTyCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 689 GGTATCATCCCTTTACTGNAACCTACAGAACCGAGACGTGTTCGAAATGTCCCGG-CCT 747
QY 221 ValValLysSerGlyAspLysProSerLeuSer 231
Db 748 GTGGTCNAATCGGAGACAAGCCCGACCTTCG 780

RESULT 6
CO646993

LOCUS

DEFINITION ILLUMIGEN_MCO_39909 Katze_MMPB2 Macaca mulatta cDNA clone
IBI0W:22761 5'-similar to Bases 4 to 915 highly similar to human
CD8A (Hs.85258), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CO646993
CO646993.1 GI:50568487
EST

Macaca mulatta (rhesus monkey)
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE
AUTHORS

1 (bases 1 to 949)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B., and
Iadonato,S.P.
Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and

TITLE

Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human

JOURNAL
PUBMED

Genome Biol. 6 (7), R60 (2005)
15998449

COMMENT

Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408

Email: cmagness@illumigen.com
Sequenced on 2004.05.27. 648 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org

PCR PRIMERS

FORWARD: CCTCACTAAAGGGAACAAA

BACKWARD: CACTATAGGCGAATTTGGTA

Insert Length: 949 Std Error: 0.00

Plate: CL000326 row: D column: 02

Seq primer: CCTCACTAAAGGGAACAAA

POLYA=No.

FEATURES

source

1..949

/organism="Macaca mulatta"

/mol_type="mRNA"

/strains="Indian"

/db_xref="taxon:9544"

/clone="IBI0W:22761"

/sex="male"

/tissue_type="blood"

/cell_type="PBMC"

/dev_stage="adult"

/lab_host="Electromax DH10B"

/clone_lib="Katze_MMPB2"

/note="Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I;

Created from CloneMiner cDNA Library Construction kit

(catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.: 9.5e-88 Length: 949
Score: 1122.00 Matches: 216
Percent Similarity: 93.2% Conservative: 5
Best Local Similarity: 91.1% Mismatches: 14
Query Match: 90.0% Indels: 2
DB: 8 Gaps: 0

US-10-804-763-1 (1-235) x CO646993 (1-949)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 56 ATGGCCCTTCCCGTGAACGCTTGTCTCTGGCGTGGTCTGTCTCCACCGCGCAGG 115
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 116 CCACACCAAGTCCGAGTGTGCGCGCTGGTCCGACCTGGAGAGCGGTGGAG 175
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 176 CTGAAGTCCAGGTCTGTCTGTCACACCGACGCTGGGTGCTGTCTTCCAGCGG 235

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 236 GCGGCGACCGCGCGCGCCACCTTCTCTATATACCTCTCCCAAAACAAGCCCAAGCGC 295
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 296 GCGAGGGCTGGACACCCACCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTC 355
 Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 356 ACCCTAGCTGACTTCCGCGCAAGAGAACGAGGGCTACTATTTCGTCTGGCCCTCAGCAAC 415
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 416 TCCATCATGTACTTTCAGCCACTTCGTGGCGGTCTTCCTGCCAGGCAAGCCACCATACG 475
 Qy 141 ProAlaProArgProProThrProAlaProThrThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 476 CCAGCGCGCGATCCCCACACCGCGGCCACACCGCGGTGCGAGCCCTGTCTCTGCGC 535
 Qy 161 ProGluLaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
 Db 536 CCAGAGGCGTCCGCGCAGCGCGGGGGCTCAGTGAACACACAGAGGGCTGGACTTCGCC 595
 Qy 181 CysAspIleTyrIleTyrAla-ProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLe 200
 Db 596 TGTGATATCTACATCTGGCGCGCCCTTGGCTGGGGCGCTTCCTTCCTTCCTGCTACT 655
 Qy 200 uValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLys-CysProArgP 220
 Db 656 GGGCATCACCTTACTGCAACACACAGAACCGAAACGTGTGGCAAAATGTCTCCAGGC 715
 Qy 220 roValValLysSerGlyAspLysProSerLeuSerAlaAlaArgTyrVal 235
 Db 716 CTGTGGTCAAAATCGGAGGCAAGCCCGCTTTCGAAAGATACGTC 762

RESULT 7
 DN997301
 LOCUS
 DEFINITION
 704 bp mRNA linear EST 17-MAY-2005
 TC111602 Human breast cancer tissue, large insert, pcwv expression
 library Homo sapiens cDNA clone TC111602 5' similar to Homo sapiens
 CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 1,
 mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 DN997301.1 GI:66257128
 EST.
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE
 AUTHORS
 1 (bases 1 to 704)
 Bickett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
 Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
 Zhang,X., Jay,G. and He,W.
 High-throughput cloning of full-length human cDNAs directly from
 cDNA libraries optimized for large and rare transcripts
 Unpublished (2005)

TITLE
 JOURNAL
 COMMENT
 Contact: Kovacs, KF
 High throughput cDNA Cloning
 Origene Technologies, Inc. (www.origene.com)
 6 Taft Court, Suite 100, Rockville, MD 20850, USA
 Tel: 301 340 3188
 Fax: 301 340 8606
 Email: cDNA@origene.com
 This EST submission is part of an on-going human full-length
 cloning project at Origene Technologies, Inc.
 Please contact Origene for access.
 Origene Technologies, Inc.
 6 Taft Ct. Suite 100
 Rockville, MD 20850
 Tel: (301) 340-3188
 http://www.origene.com

Seq primer: pcwv6 5prime forward vector primer, OriGene
 Technologies Inc.
 Location/Qualifiers
 1..704
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TC111602"
 /tissue_type="Breast cancer"
 /clone_lib="Human breast cancer tissue, large insert, pcwv
 expression library"
 /note="Organ: Mammary gland (cancer tissue); Vector:
 pcwv6-XL5; Site 1: EcoRI; Site 2: XhoI/SalI compatible end
 ligatio; Oligo-dT primed reverse transcription optimized
 for large and GC rich mRNA transcripts, cDNA size
 selection, optimized ligation for large inserts into
 mammalian expression vector, random clones selected for
 end sequence verification of full-length genes"

ORIGIN

Alignment Scores:
 Pred. No.: 5.85e-87 Length: 704
 Score: 1111.00 Matches: 210
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 89.1% Indels: 0
 DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x DN997301 (1-704)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 Db 70 ATGGCCCTTACCAGTGACCGCCTTCTCTCGCGTGGCCTTGGCTCCACGCCCGCAGG 129
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 130 CCGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGGCGAGACATGGAG 189
 Qy 41 LeuLysCysGlnValLeuLeuLeuSerAsnProThrSerGlyCysSerTrpPheGlnPro 60
 Db 190 CTGAAGTGCCAGGTGCTGCTCCAAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 249
 Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 250 GCGCGCGCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 309
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 310 GCGAGGGCTGGACACCCACCGGTCTTCGGGCAAGAGTTGGGGGACACCTTCGTCTC 369
 Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 370 ACCCTGAGCGACTTCCGCGCAGAGAACGAGGGCTACTATTTCGTCTGGCCCTCAGCAAC 429
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 430 TCCATCATGTACTTTCAGCCACTTCGTGGCGGTTCCTGCCAGGCAAGCCACCATCAGC 489
 Qy 141 ProAlaProArgProProThrProAlaProThrThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 490 CCAGCGCGCGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCTCTGCGC 549
 Qy 161 ProGluLaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
 Db 550 CCAGAGGCGTCCGCGCCACGCGCGGCGCAGTGCAACAGGGGGCTGGACTTCGCC 609
 Qy 181 CysAspIleTyrIleTyrAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
 Db 610 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTACTG 669
 Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArg 211
 Db 670 GTTATCACCTTTTACTGCAACACACAGGAACCGA 702

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RESULT 8
BI911195
LOCUS 603062918F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5211989 5',
DEFINITION mRNA sequence.
ACCESSION BI911195
VERSION BI911195.1 GI:16174808
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 796)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11532 row: d column: 06
High quality sequence start: 29
High quality sequence stop: 791.
FEATURES
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    location/Qualifiers
    1..796
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    /clone="IMAGE:5211989"
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    /lab_host="DH10B"
    /clone_lib="NIH_MGC_118"
    /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
    (destroyed); RNA source leukocytes from anonymous pool of
    non-activated adult donors. Library is oligo-dT primed
    and directionally cloned (EcoRV site is destroyed upon
    cloning). Average insert size 1.7 kb, insert size range
    1.2-3.3 kb. Library is normalized and enriched for
    full-length clones and was constructed by C. Gruber
    (Invitrogen). Research Genetics tracking code 027. Note:
    this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 3,89e-85 Length: 796
Score: 1091.00 Matches: 217
Percent Similarity: 98.2% Conservative: 0
Best Local Similarity: 98.2% Mismatches: 1
Query Match: 87.5% Indels: 4
DB: 2 Gaps: 0

US-10-804-763-1 (1-235) x BI911195 (1-796)

QY 1 MetAlaLeuProValThraLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 140 ATGGCCCTTACCAGTACCGCCCTTGCTCTCGCTGGCCCTTGCTGCTCCACGCCCGCAGG 199
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 200 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGGACTGGAACTGGCGGAGACGTGGAG 259
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 260 CTGAAGTCCAGGTCTGCTGCTCCAAACCGAGCTGGGCTGCTGGTCTCTCCAGCGG 319
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80

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Db 320 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAGCCCAAGCG 379
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 380 GCGGAGGGGCTGACACCCAGCGGTTCTCGGGCAAGAGGTGGGGACACCTTCGTCCTC 439
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyPheCysSerAlaLeuSerAsn 120
DB 440 ACCCTGAGCGACTTCGCCCGAGAGAACGAGGGCTACTATTCTTGCTCGGCCCTGAGCAAC 499
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 500 TCCATCATGTACTTACGCCACTTCGTGCGCGTCTTCTGCGCAGCAAGCCACGACG 559
QY 141 ProAlaProArgProProThrProAla-ProThrIleAlaSerGlnProLeuSerLeuAr 160
DB 560 CCAGCGCCGAGACCAACACCGGCTGCCACCATCGCGTGCAGCCCCCTGTCCTGCG 619
QY 160 gProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAl 180
DB 620 CCCAGAGGGCTGCCGCCAGCGCGCGCGCGCAGTGCCACACGAGGGGCTGCACTTCG 679
QY 180 a-CysAspIleTyrIleTrpAlaProLeuAla-GlyThrCysGlyValLeuLeuSer 199
DB 680 CCGTGATATCTACATCTGGGCGCCCTTGGCCCGGACTTGTGGGTCTCTTCTCTGTC 739
QY 200 LeuValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysPro 218
DB 740 CTGGTTATCACCTTTACTTG-AACCACAGAAACCGAAGACGTGTTTGCAATGTCCC 795

RESULT 9
BI935165
LOCUS 603088746F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5227906 5',
DEFINITION mRNA sequence.
ACCESSION BI935165
VERSION BI935165.1 GI:15946715
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 840)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11573 row: k column: 11
High quality sequence stop: 639.
FEATURES
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    /organism="Homo sapiens"
    /mol_type="mRNA"
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    /clone="IMAGE:5227906"
    /lab_host="DH10B"
    /clone_lib="NIH_MGC_120"
    /note="Organ: pooled pancreas and spleen; Vector:
    pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
    source anonymous pool of spleen and pancreas from 28 yo
    male. Library is oligo-dT primed and directionally cloned
    (EcoRV site is destroyed upon cloning). Average insert
    size 1.5 kb, insert size range 1-2.5 kb. Library is

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QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 459 TCCATCATGACTTACAGCACTTCGTGCGGCTTCTCTGCCAGGAAGCCACCAAGC 518

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 519 CCAGCGCGCGACCCACACACCGGCGCCCATCGCTCGAGCCCTGTCCCTGCGC 578

QY 161 ProGluAlaCyArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 579 CCAGAGCGGTGCGCGCGACCGCGCGGCGCGAGTGCAACAGAGGGGTGGACTTCGCC 638

QY 181 CysAspIleTyIleTTP-AlaProLeuAla-GlyThrCysGlyValLeu-LeuLeu-Se 199
Db 639 TGTGATATCTACATCTGGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTCGTGC 698

QY 199 rLeuValIleThrLeuTyCysAsnHisArgAsnArgArgVal 214
Db 699 ACTGGTTACCCCTTACTGCAACCAACAGTAAGTCCCGAGGAATC 744

RESULT 11
LOCUS DA946587 580 bp mRNA linear EST 03-DEC-2005
DEFINITION DA946587 SPLEN2 Homo sapiens cDNA clone SPLEN2022409 5', mRNA
sequence.
ACCESSION DA946587.1 GI:83054667
VERSION DA946587
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saiko,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.

FEATURES
Location/Qualifiers
1..580
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="SPLEN2022409"
/tissue_type="spleen"
/clone_lib="SPLEN2"
/note="Vector: pME18SFL3"

ORIGIN
Alignment Scores: 4.73e-78 Length: 580
Pred. No.: 1008.00 Matches: 192
Score: 99.5% Conservative: 1
Percent Similarity:

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Best Local Similarity: 99.0% Mismatches: 0
Query Match: 80.8% Indels: 1
DB: 9 Gaps: 0

US-10-804-763-1 (1-235) x DA946587 (1-580)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAArg 20
Db 1 ATGGGCTTACCAGTACCGCCCTTGTCTGCGGCTGGCCTTGTCTCCACGCGCAGG 60

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGly-GluThrValGI 40
Db 61 CCAGGCCAGTTCGGGGTFCGCCGTGGATCGGACTGGAACTGGGCTCGAGACAGTGA 120

QY 40 uLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPr 60
Db 121 GTGAAGTGCAGGTGCTGTCCAAACCCGAGCTGGGCTGCTGTGGCTCTTCAGGC 180

QY 60 oArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrLeuSerGlnAsnLysProLysAl 80
Db 181 GCGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAACAGGCCAAGGC 240

QY 80 aAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValle 100
Db 241 GCGCGAGGGGTGGACACCCAGCGTTCCTCGGGCAAGAGGTTGGGGGACACCTTCGTC 300

QY 100 uThrLeuSerAspPheArgGluAsnGluGlyTyTrPheCysSerAlaLeuSerAs 120
Db 301 CACCTTGAGGACTTCCCGCGGAGAGAACGAGGGCTACTATTTCCTCGGCCCTGAGCAA 360

QY 120 nSerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 361 CTCATCATGACTTTCAGCCACTTCGTGCGGCTCTTCTGCGCAGGAGGCCACACGAC 420

QY 140 rProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuAr 160
Db 421 GCCAGCGCGCGACCAACCAACACCGCGGCCACCACTCGCGTCGACGCCCTGTCTGCC 480

QY 160 gProGluAlaCyAsGProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAl 180
Db 481 CCCAGAGGGTGGCGGCCAGCGGGGGGGCGCATGTGCACAGGGGGCTGGACTTCGC 540

QY 180 aCysAspIleTyIleTrpAlaProLeuAlaGlyThrCys 193
Db 541 CTGTGATATCTACATCTGGCGGCGCTTCGCGGAGCTTGT 580

RESULT 12
LOCUS CR619549 1948 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI070YG17 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR619549
VERSION CR619549.1 GI:50500356
KEYWORDS HTC; CNSLT.cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1948)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1948)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
REFERENCE
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
REMARK BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

source
1..1948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI070YG17"
/tissue_type="Placenta Cot 25-normalized"
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ORIGIN

Alignment Scores:

Pred. No.: 3.25e-77 Length: 1948
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 80.7% Indels: 37
DB: 6 Gaps: 1

US-10-804-763-1 (1-235) x CR619549 (1-1948)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 71 ATGGCCTTACCAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 130
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 131 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGACCTGGAACTGGGGGAGACAGTGGAG 190
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 191 CTGAAGTCCAGGTGCTGTGTCCAAACCGAGCTCGGGCTGCTGTGCTCTTCAGCGC 250
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 251 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGC 310
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 311 GCCGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGAGACACTTTCGTCTC 370
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 371 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCTGAGCAAC 430
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 431 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTGCCAGCGAAGCCACCAACG 490
Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 491 CCAGCGCGGACCAACACCGCGGCCACCATCGGCTGCGCCCTGTCCTCGGCGC 550
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
Db 551 CCAGAGGCGTGCAGCGCGCGGGGGCGCA----- 583
Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuLeuSerLeu 200
Db 583 ----- 583
Qy 201 ValIleThrLeuTyrCysAsnHisArgAsnArgArgValCysLysCysProArgPro 220
Db 584 -----GGGAACCGAGACGTGTTGCAANTGTCCTCCCGGCT 619
Qy 221 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
Db 620 GTGGTCAATCGGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 664

RESULT 13

DR007174

LOCUS

DEFINITION

DR007174 755 bp mRNA linear EST 17-MAY-2005
TC101240 Human spleen, large insert, pCMV expression library Homo sapiens cDNA clone TC101240 5' similar to Homo sapiens CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 2, mRNA sequence.

ACCESSION

DR007174 GI:66267047

VERSION

DR007174.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE

1 (bases 1 to 755)

AUTHORS

Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.

TITLE

High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts

JOURNAL

Unpublished (2005)

COMMENT

Contact: Kovacs, KF

High Throughput cDNA Cloning

OriGene Technologies, Inc. (www.origene.com)

6 Taft Court, Suite 100, Rockville, MD 20850, USA

Tel: 301 340 3188

Fax: 301 340 8606

Email: cDNA@origene.com

This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.

Please contact OriGene for access.

OriGene Technologies, Inc.

6 Taft Ct. Suite 100

Rockville, MD 20850

Tel: (301) 340-3188

http://www.origene.com

Seq primer: pCMV6 Sprime forward vector primer, OriGene

Technologies Inc.

FEATURES

Location/Qualifiers

1..755

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TC101240"

/tissue_type="Spleen"

/clone_lib="Human spleen, large insert, pCMV expression
library"

/note="Organ: Spleen; Vector: pCMV6-XL4; Site 1: EcoRI;
Site 2: XhoI/SalI compatible end ligatio; Oligo-dT primed
reverse transcription optimized for large and GC rich mRNA
transcripts, cDNA size selection, optimized ligation for
large inserts into mammalian expression vector, random
clones selected for end sequence verification of
full-length genes"

ORIGIN

Alignment Scores:

Pred. No.: 3.06e-77 Length: 755
Score: 1000.50 Matches: 198
Percent Similarity: 83.9% Conservative: 0
Best Local Similarity: 83.9% Mismatches: 0
Query Match: 80.2% Indels: 38
DB: 9 Gaps: 1

US-10-804-763-1 (1-235) x DR007174 (1-755)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

Db 37 ATGGCCTTACCAGTACCGCCCTTGCTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 96

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

Db 97 CCGAGCCAGTTCCGGGTGTCGGCTGATCGACCTGGACCTGGGCGAGACAGTGGAG 156

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

Location/Qualifiers
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="THYMU2034397"
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ORIGIN

Alignment Scores:
 Pred. No.: 2,31e-77 Length: 569
 Score: 1000.00 Matches: 188
 Percent Similarity: 99.5% Conservative: 0
 Best Local Similarity: 99.5% Mismatches: 1
 Query Match: 80.2% Indels: 0
 DB: Gaps: 0

US-10-804-763-1 (1-235) x DB124972 (1-569)

Qy 5 ValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSerGlnPhe 24
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 Db 2 GTGACCGCCTTCTCTCGCGCTGGCTTGTCTCCAGCGCGCCAGCGCCAGTTC 61
 |||||
 Qy 25 ArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln 44
 |||||
 Db 62 CGGGTGTGCGCGCTGGATCGGACCTGGAACTTGGCGGACAGTGGAGCTGAAGTCCAG 121
 |||||
 Qy 45 ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGlyAlaAla 64
 |||||
 Db 122 GTGCTGTGTCTCAACCGCAGCTCGGGCTGCTCGTGGCTTTCAGCGCGCGCGCGCC 181
 |||||
 Qy 65 AlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysValAlaGluGlyLeu 84
 |||||
 Db 182 GCCAGTCCCACTTCTCTCTTACCTCTCCAAAACAAGCCCAAGCGCGCGCGGGGTG 241
 |||||
 Qy 85 AspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeuSerAsp 104
 |||||
 Db 242 GACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCTCTCCTCACCCTGAGCGAC 301
 |||||
 Qy 105 PheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsnSerIleMetTyr 124
 |||||
 Db 302 TTCCGCGCAGAGACAGAGGGCTACTATTCTGCGCGCGCTGAGCAACTCCATCATGTAC 361
 |||||
 Qy 125 PheSerHisPheValProValPheLeuProAlaLysProThrThrProAlaProArg 144
 |||||
 Db 362 TTCACCACTTCTGCGCGGCTCTTCTGCGAGGAAAGCCACCAGCGCGCGCGCGA 421
 |||||
 Qy 145 PropThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGluAlaCys 164
 |||||
 Db 422 CCACCAACACCGCGCGCCACCATCGGTGCGAGCCCTTCTCTGCGCCAGAGGGGTGC 481
 |||||
 Qy 165 ArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAlaCysAspIleTyr 184
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 Db 482 CGGCAGCGCGCGGGGGCGCAGTCACACGAGGGGGTGGACTTCGCTGTGATATCTAC 541
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 Qy 185 IleTrpAlaProLeuAlaGlyThrCys 193
 |||||
 Db 542 ATCTGGCGCGCCTTGGCGGGACTTGT 568
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RESULT 15
 DA958887
 LOCUS
 DEFINITION
 ACCESSION

DA958887 555 bp mRNA linear EST 11-NOV-2005
 DA958887 SPLEN2 Homo sapiens cDNA clone SPLEN2038708 5', mRNA
 sequence.

DA958887

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
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 Db 157 CTGAAGTGCAGGTGCTGTCTCAACCCGACGTCGGGTCTCGTGGCTCTTCCAGCGC 216
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 Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
 |||||
 Db 217 CGCGCGCGCGCGCGCGCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 276
 |||||
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
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 Db 277 GCCAGAGGGCTGACACCCAGCGGTTCTCGGCAAGAGTGTGGGACACCTTCTGTCCTC 336
 |||||
 Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
 |||||
 Db 337 ACCCTGAGCGACTTCGCGCAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 396
 |||||
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
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 Db 397 TCCATCATGTACTTTCAGCCACTTCTGTCGGCTTCTCTGCGCAAGCCCAAGCGCG 456
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 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
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 |||||
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaValHisThrArgGlyLeuAspPheAla 180
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 Db 517 CCAGAGCGGTGCGCGCAGCGCGCGGGCGCT----- 549
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 Qy 181 CysAspIleTyrIleTrpAlaProLeuAlaGlyThrCysGlyValLeuLeuSerLeu 200
 |||||
 Db 549 ----- 549
 |||||
 Qy 201 ValIleThrLeuTyrCysAsnHisArg-AsnArgArgArgValCysLysCysProArgPr 220
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 Db 550 -----AGGAAACCGAAGACGTGTTTGCAATGTCCTCCCGGCC 585
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 Qy 220 oValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 235
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 Db 586 TGTGGTCAAAATCGGAGACAAGCCAGCTTTTCGGCGGAGATAGTC 631
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RESULT 14

DB124972 569 bp mRNA linear EST 04-DEC-2005
 DB124972 THYMU2 Homo sapiens cDNA clone THYMU2034397 5', mRNA
 sequence.

ACCESSION

DB124972

VERSION

DB124972.1 GI:83212682

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 569)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,

Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,

Yonoyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,

Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,

Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

16344560

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

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JOURNAL

PUBLISHED

COMMENT

```

VERSION DA958887.1 GI:82064474
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo;
1. (bases 1 to 555)
REFERENCE
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Teuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatauma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Sugano,S.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,F. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
JOURNAL 16344560
PUBMED
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES
source
Location/Qualifiers
1..555
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="SPLN2038708"
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ORIGIN
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 78.8% Indels: 0
DB: 9 Gaps: 0
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Qy 14 LeuLeuLeuHisAlaAlaArgProSerGlnPheArgValSerProLeuAspArgThrTrp 33
Db 3 TTGCTGCTCCAGCGCCGAGCCGAGCGGAGTCCCGGGTGTCCCGCTGGATCGGACCTGG 62
Qy 34 AsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly 53
Db 63 AACCTGGGGGAGACAGTGGAGCTGAAGTGCACAGTGTCTGTCTCAACCCGACGTCGGGC 122
Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db 123 TGCTCGTGGCTCTTCAGCGCGCGCGCGCGCGCGCGCGCTCCACCTTCCTCTATACCTC 182
Qy 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 183 TCCCAAAACAGCCCAAGCGCCGAGGGGCTGGACACCCAGCGGTTTTCGGGCAAGAGG 242
Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyr 113
Db 243 TTGGGGGACACCTTCCTCTCCTACCTTGAGCGACTTCCGCGGAGAGACGAGGGCTACTAT 302

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Search completed: May 30, 2006, 06:51:25
Job time : 5113.67 secs

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Qy 114 PheCysSerAlaLeuSerAsnSerIleMetTyrPheSerHisPheValProValPheLeu 133
Db 303 TTCTGCTCGGCCCTTGAGCAACTCCATCATGTACTTCAGCCACTTCGTGCCGTCTCTCG 362
Qy 134 ProAlaLysProThrThrThrProAlaProArgProProThrProAlaProThrIleAla 153
Db 363 CCAGCGAAGCCACACGACGCGCGCGGACCAACACCGCGGCCCCACCATCGGG 422
Qy 154 SerGlnProLeuSerLeuArgProGluAlaCysArgProAlaAlaGlyGlyAlaValHis 173
Db 423 TCGCAGCCCTGTCCCTGCGCCACAGAGCGGTGCGGCGCGGCGGGGGCGGAGTGCAC 482
Qy 174 ThrArgGlyLeuAspPheAlaCysAspIleTyrIleTTPAlaProLeuAlaGlyThrCys 193
Db 483 ACGAGGGGGCTGGAGCTTCGCCCTGTGATATCTACATCTGGGCGCCCTTGCGCGGACTTGT 542
Qy 194 GlyValLeuLeu 197
Db 543 GGGGTCTCTCTC 554

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|--|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|

by

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ACCESSION CQ843147
VERSION CQ843147.1 GI:50894934

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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1 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J., Isono,Y., Nagai,K. and Irie,R.
Full-length human cdna
Patent: EP 1440981-A 1794 28-JUL-2004;
Research Association for Biotechnology (JP)

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source

1..3048

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

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ACCESSION AK124156
VERSION AK124156.1 GI:34529876
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
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Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K.,
Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
Sugano, S., Negahari, K., Maeno, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
UNpublished
2 (bases 1 to 3048)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail: flj-cdna@nifty.com, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: Reverse Proteomics Research Institute, HRI and
RAB.
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ORIGIN
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Matches 2134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 781 TGGTCAATCGGGAGACAAAGCCGAGCTTTTGGGAGAGATAGTCTAAACCTGTGCAACAG 840
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| QY | 1081 | CAGGCAGAGCTACCGCGAGAGTTCTCAGAAATCATCTGAGAGAGCTGGAGGCACCCATG | 1140 |
| Db | 1993 | CAGGCAGAGCTACCGCGAGAGTTCTCAGAAATCATCTGAGAGAGCTGGAGGCACCCATG | 2052 |
| QY | 1141 | CAATCTCAACTCTTCCCGCGCGTTTTCACAAAGGGGAGGCTTAAGCCAGAGACAGCT | 1200 |
| Db | 2053 | CGGTCTCAACTCTTCCCGCGCGTTTTCACAAAGGGGAGGCTTAAGCCAGAGACAGCT | 2112 |
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| Db | 2113 | TGATCAAGGACACAGCAAGTCAAGGTTGGAGCAGTACGTGGAGGACCTTGTCTCCCA | 2172 |
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| Db | 2593 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGATCACTGATGA | 2652 |
| QY | 1741 | CTTTTATATCTTTGTAAGACAATTTGAGAGGCCCTCACAGCCCTGGCCTCTGCT | 1800 |
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| QY | 1801 | CAACTAGCAGATACAGGGATGAGGACCTCAGCTCTCTTAAGGAGGCTGAGAGCCCAA | 1860 |
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| QY | 1861 | CTGCTGTCCCAACATGCACTTCTCTTGTCTTAAGGTATGTAACAAGCAATGCCTGCCATT | 1920 |
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| QY | 1921 | GGAGAGAAAACTTAAGTAGATAGGAAATAGAACCACTCATTAATCTTCACCTTAGG | 1980 |
| Db | 2833 | GGAGAGAAAACTTAAGTAGATAGGAAATAGAACCACTCATTAATCTTCACCTTAGG | 2892 |
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| | |
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| RESULT | 4 |
| BC025715 | |
| LOCUS | |
| DEFINITION | Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript variant 1, mRNA (CDNA clone MGC:34614 IMAGE:5227906), complete cds. |
| ACCESSION | BC025715 |
| VERSION | BC025715.1 |
| KEYWORDS | GI:19344021 |
| SOURCE | MGC. |
| ORGANISM | Homo sapiens (human) |
| REFERENCE | 1 (bases 1 to 2150) |
| AUTHORS | Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,J.A., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Rodrigues,S., Bouffard,G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalek,U., Smalls,D.E., Schenck,A., Schein,J.E., Jones,S.J. and Marra,M.A. |
| TITLE | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences |
| JOURNAL | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) |
| PUBMED | 12477932 |
| REFERENCE | 2 (bases 1 to 2150) |
| AUTHORS | Strausberg,R. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA |
| REMARK | NIH-MGC Project URL: http://mgc.nci.nih.gov |
| COMMENT | Contact: MGC help desk Email: cgabps@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisec.nih.gov/ Contact: nisc.mgc@nih.gov Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Iaric,P., Legaspi,R., Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D. |

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAX plate: 49 Row: 0 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA g1: 2788641.

FEATURES
source

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ORIGIN

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| Qy | 235 | TGGAGCTGAAGTGCACAGTGTCTGTCCAAACCGAGTGGGCTGCTCGTGGCTCTTCC | 294 | |
| Db | 121 | TGGAGCTGAAGTGCACAGTGTCTGTCTCAAACCGAGTGGGCTGCTCGTGGCTCTTCC | 180 | |
| Qy | 295 | AGCCGCGCGCGCGCCAGTCCACCTTCTCTCTATACCTCTCCCAAACAAAGCCCA | 354 | |
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RESULT 5
LOCUS CQ882012 2150 bp DNA linear PAT 11-OCT-2004
DEFINITION Sequence 4 from Patent WO2004083404.
ACCESSION CQ882012
VERSION CQ882012.1 GI:54034737
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Qi, Y., Zhang, X. and Konigsberg, P.J.
AUTHORS Gene therapy vectors having reduced immunogenicity
TITLE Patent: WO 2004083404-A 4 30-SEP-2004;
JOURNAL Isogenis, Inc. (US)
FEATURES
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ORIGIN
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RESULT 6
AK097942
LOCUS
DEFINITION
Homo sapiens CDNA FLJ40623 fis, clone THYMU2013863, highly similar to T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA CHAIN PRECURSOR.
ACCESSION
AK097942.1 GI:21757848
VERSION
oligo capping; fis (full insert sequence).
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohbayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Iehi, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hotcu, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Hara, H., Tanase, T. O., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, N., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshihara, Y., Matsunawa, H., Ichihara, T., Shiohara, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Maehuo, Y., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length human cDNAs
Nat. Genet. 36 (1), 40-45 (2004)
2
Nishi, T., Ota, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Maehuo, Y., Nagai, K. and Isogai, T.
NEO human cDNA sequencing project
Unpublished
3 (bases 1 to 2090)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu Chiba 292-0812, Japan (E-mail: filj-cdn@nifty.com, tel:81-438-52-3975, Fax:81-438-52-3986)
NEO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
Location/Qualifiers
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DEFINITION
ACCESSION M12824
VERSION M12824.1 GI:339426
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE 1 (bases 1 to 1975)
AUTHORS Sukhatme,V.P., Sizer,K.C., Vollmer,A.C., Hunkapiller,T. and
Parnes,J.R.
TITLE The T cell differentiation antigen Leu-2/T8 is homologous to
immunoglobulin and T cell receptor variable regions
JOURNAL Cell 40 (3), 591-597 (1985)
PUBMED 3918796
COMMENT Original source text: Human, cDNA to mRNA, clone pL2-M.
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Db 1201 GCAGTAGCTGGAGGACCTTGTCTCCAGCTCAGGGCTCTTTCTCCACACCACTTCAGGT 1260
QY 1293 CTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTCTTGAGTCTCCAAAGGCGGAAGAAC 1352
Db 1261 CTTTCTTTCCGAGGCCCTGTCTCAGGGTGAGGTCTTGAGTCTCCAAAGGCGGAAGAAC 1320
QY 1353 AAGTACTCTTGTATACCTGGGATACCTGTGCCAGAGCTCGAGGAGGTAAATGAATAAG 1412
Db 1321 AAGTACTCTTGTATACCTGGGATACCTGTGCCAGAGCTCGAGGAGGTAAATGAATAAG 1380
QY 1413 AAGAGAACTGCCTTTGGCAGAGTCTTATAATGTAAACAATATCAGACTTTTTTTTTTAT 1472
Db 1381 AAGAGAACTGCCTTTGGCAGAGTCTTATAATGTAAACAATATCAGACTTTTTTTTTTAT 1440
QY 1473 AATCAAGCTTAAATTTGTATAGACCTTAAATGAATGAAGTGTGAGCTTAACCTCGGAA 1532
Db 1441 AATCAAGCTTAAATTTGTATAGACCTTAAATGAATGAAGTGTGAGCTTAACCTCGGAA 1500
QY 1533 AATGAATCCCTCTATCTCTAAAGAAATCTCTGTGAAACCCCTATCTGGAGGCGGAATTG 1592
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QY 1593 CTCTCCAGCCCTTGCATTCGAGAGGGGCCATGAAGAGGACAGGCTACCCCTTTACAA 1652
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Db 1621 ATAGAATTTGAGCATCAGTGAGGTTAACTAAGGCCCTCTTGAATCTCTGAATTTGAGAT 1680
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QY 1773 AGCCCTCTCACAGCCCTGGCCTCTGCTCAACTAGCAGATACAGGATGAGGACAGACCTG 1832
Db 1741 AGCCCTCTCACAGCCCTGGCCTCTGCTCAACTAGCAGATACAGGATGAGGACAGACCTG 1800
QY 1833 ACTCTCTTAAGAGGCTGAGAGGCCAACTGCTGTCTCCAAACATGCACTTCTCTGTTAA 1892
Db 1801 ACTCTCTTAAGAGGCTGAGAGGCCAACTGCTGTCTCCAAACATGCACTTCTCTGTTAA 1860
QY 1893 GGTATGTCACAGCATGCTGCCATTCGAGAGGAAACTTAACTAGTAGATAGGAAATA 1952
Db 1861 GGTATGTCACAGCATGCTGCCATTCGAGAGGAAACTTAACTAGTAGATAGGAAATA 1920
QY 1953 AGAACCACTCATAATTTCTTACCTTAGGAATAATCTCTGTTAAATATGTTGATACA 2007
Db 1921 AGAACCACTCATAATTTCTTACCTTAGGAATAATCTCTGTTAAATATGTTGATACA 1975

RESULT 8

AC064848
LOCUS AC064848 135809 bp DNA linear PRI 15-APR-2005
DEFINITION Homo sapiens BAC clone RP11-81F3 from 2, complete sequence.
ACCESSION AC064848
VERSION AC064848.5 GI:15638742
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 135809)
AUTHORS Kruchowski, S., Haakenson, W. and Boyer, E.
TITLE The sequence of Homo sapiens BAC clone RP11-81F3
JOURNAL Unpublished (2001)
REFERENCE 2 (bases 1 to 135809)
AUTHORS Waterston, R.H.

TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNALREFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (23-APR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 135809)
Waterston, R.H.
Direct Submission
Submitted (18-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 135809)
Waterston, R.
Direct Submission
Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 135809)
Wilson, R.K.
Direct Submission
Submitted (15-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 18, 2001 this sequence version replaced gi:13592273.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: submissions@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH0081F03

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-269K22, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-81F3; actual end is at base position 34458 of RP11-269K22.

RP11-81F3 from base positions 17803 to 18103 and 101913 to 101968 are represented by sequence derived from PCR.

FEATURES
source

Location/Qualifiers
1. .135809
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-81F3"
/clone_lib="RPCI-11"
576. .806

misc_feature

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Qy 1659 TTTGAGCATCAGTGAGGTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAAC 1718
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Qy 1719 ATGTTCTCGGATCAGTGAGCTTTTATCTTTGAAAGACAAATTGTTGGAGGCC 1778
Db 1247 ATGTTCTCGGATCAGTGAGCTTTTATCTTTGAAAGACAAATTGTTGGAGGCC 1306
Qy 1779 TCACAGACCCCTGGCTCTCACTAGCAGATACAGGATGAGGCAGCCTGACTCTC 1838
Db 1307 TCACAGACCCCTGGCTCTCACTAGCAGATACAGGATGAGGCAGCCTGACTCTC 1366
Qy 1839 TTAAGGAGGCTGAGAGCCCAACTGCTGCTCCCAACATGCACTTCCCTTGAAGGTATG 1898
Db 1367 TTAAGGAGGCTGAGAGCCCAACTGCTGCTCCCAACATGCACTTCCCTTGAAGGTATG 1426
Qy 1899 GTAAGAAGTCTGCTGCCCTTGAGAGAAACCTTAAGTAGATAGGAATAAGAAC 1958
Db 1427 GTACAAGCAATGCTGCCCTTGAGAGAAACCTTAAGTAGATAGGAATAAGAAC 1486
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Db 1487 ACTCATATCTTACCTTAGAATACTCCTGTTAATATGTTGATCATCTTCCCTGAT 1546
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Db 1547 TATTTTACACATACATGTAATAATATCTCTTTTAAATAGGCTTGAATGCT 1606
Qy 2079 GTTAGAGTGGCTTAAATGAATAACATTTGTAGATCCTCTTAAATGGGTAACAGCA 2137
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RESULT 10
HUMHCD8A HUMHCD8A 7319 bp DNA linear PRI 07-JAN-1995
LOCUS Human MHC class I CD8 alpha-chain (Leu-2/T8) gene, complete cds.
DEFINITION
ACCESSION M27161
VERSION
KEYWORDS cell surface antigen; cell surface glycoprotein; class I gene; integral membrane protein; major histocompatibility complex.

SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 7319)
AUTHORS Nakayama,K., Tokito,S., Okumura,K. and Nakauchi,H.
TITLE Structure and expression of the gene encoding CD8 alpha chain (Leu-2/T8)
JOURNAL Immunogenetics 30 (5), 393-397 (1989)
PUBMED 2509342
COMMENT Original source text: Human DNA, clone pLE2B13.5.
Draft entry and computer-readable sequence for [1] kindly submitted by K.-i.Nakayama, 31-AUG-1989.

FEATURES
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/db_xref="taxon:9606"
/map="2p12"

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/note="MHC CD8 alpha-chain mRNA and introns"

misc_feature
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/note="Tcr v-beta decamer-like sequence"
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/db_xref="GI:386908"
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exon 763..1116
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intron 1117..1699
/note="CD8 alpha-chain intron B"
exon 1700..1810
/number=3
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/note="CD8 intron C"
exon 2017..2127
/number=4
intron 2128..2889
/note="CD8 intron D"
exon 2890..2920
/number=5
intron 2921..5503
/note="CD8 intron E"
exon 5504..5555
/note="MHC CD8 alpha-chain (Leu-2/T8)"
/number=6
ORIGIN 1 bp upstream of HindIII site; chromosome 2p12.

Query Match 59.4%; Score 1343; DB 5; Length 7319;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1363; Conservative 0; Mismatches 16; Indels 1; Gaps 1;
Qy 759 GTTTGCAAAATGTCCTCCCGGCTGTGTCATAATCGGGAGACAAGCCAGCGCTTTCGGCGAGA 818
Db 5487 GCTTTCCTCTCTTCAGGCTGTGTCATAATCGGGAGACAAGCCAGCGCTTTCGGCGAGA 5546
Qy 819 TACGCTAACCTGTGCAACGCCACTACATTACTTCAAACTGAGATCCTTCCTTTTGGAG 878
Db 5547 TACGCTAACCTGTGCAACGCCACTACATTACTTCAAACTGAGATCCTTCCTTTTGGAG 5606
Qy 879 GGAGCAAGTCTCTCCCTTTCATTTTTCAGTCTTCCTCCCTGCTGATTCATCTCATGA 938
Db 5607 GGAGCAAGTCTCTCCCTTTCATTTTTCAGTCTTCCTCCCTGCTGATTCATCTCATGA 5666
Qy 939 TTATTATTTAGTGGGGGGGGTGGGAAAGATTACTTTTCTTTATGTTGTGACGGGA 998
Db 5667 TTATTATTTAGTGGGGGGGGTGGGAAAGATTACTTTTCTTTATGTTGTGACGGGA 5726
Qy 999 AACAAAACTAGGTAAAATCTACAGTACACCAAGGGGTCACAATACTGTGTGCGCACAT 1058
Db 5727 AACAAAACTAGGTAAAATCTACAGTACACCAAGGGGTCACAATACTGTGTGCGCACAT 5786
Qy 1059 CGCGTAGGGGTGGAAGGGGCGAGCCAGAGCTACCCGAGAGTTCTCAGAAATCATGCT 1118
Db 5787 CGCGTAGGGGTGGAAGGGGCGAGCTACCCGAGAGTTCTCAGAAATCATGCT 5846
Qy 1119 GAGAGAGCTGGAGGCCACCCATGCCATCTCAACCTCTTCCCGCCCGTTTACAAAGGGGG 1178

Db 5847 GAGAGAGCTGGAGGCCACCATGCAATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGG 5906
QY 1179 AGGCTAAAGCCAGAGACAGCTTGATCAAGGCGACACAGCACTCAGGTTGGAGCAGTA 1238
Db 5907 AGGCTAAAGCCAGAGACAGCTTGATCAAGGCGACACAGCACTCAGGTTGGAGCAGTA 5966
QY 1239 GCTGGAGGACCTTGTCTCCAGCTCAGGCTCTTCCCTCCACACCACTCAGCTCTTCT 1298
Db 5967 GCTGGAGGACCTTGTCTCCAGCTCAGGCTCTTCCCTCCACACCACTCAGCTCTTCT 6026
QY 1299 TTCCGAGGCCCTGTCTCAGGCTGAGTCTCAGTCTCCACGCAAGGACACAGTAC 1358
Db 6027 TTCCGAGGCCCTGTCTCAGGCTGAGTCTCAGTCTCCACGCAAGGACACAGTAC 6086
QY 1359 TTCTTGATACCTGGGATACCTGTGCCAGAGCTTCGAGGAGGTAATGAATTAAGAGAGA 1418
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QY 1478 AGCTTAAATTTGTATAGACCTTAAATGAATGAATGAATGAATGAATGAATGAATGA 1537
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QY 1598 CCAGCCCTTGCATTCAGAGGGGCCCATGAAGAGAGACAGGCTACCCCTTTACAAATGA 1657
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QY 1658 ATTGAGCATGAGTGAAGTTAACTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAA 1717
Db 6387 ATTGAGCATGAGTGAAGTTAACTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAA 6446
QY 1718 CATGTTCTGGGATCACTGATGACTTTTATATCTTTGTAAGACAAATTTGGAGAGCC 1777
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QY 1778 CTCACAGCCCTGGCTCTGCTCAACTAGCAGATACAGGATAGGAGACGCTGACTCT 1837
Db 6507 ATCACAGCCCTGGCTCTGCTCAACTAGCAGATACAGGATAGGAGACGCTGACTCT 6566
QY 1838 CTTAAGGAGGCTGAGAGCCCAACTGCTGCCCAACATGCACTTCTTCTTAAAGTAT 1897
Db 6567 CTTAAGGAGGCTGAGAGCCCAACTGCTGCCCAACATGCACTTCTTCTTAAAGTAT 6626
QY 1898 GGTACAAGCAATGCTGCTGCCCATTTGGAGAGAAAAAATCTTAAGTAGATAAGGAAATAAGAAC 1957
Db 6627 GGTACAAGCAATGCTGCTGCCCATTTGGAGAGAAAAAATCTTAAGTAGATAAGGAAATAAGAAC 6686
QY 1958 CACTCATATTTCTACCTTAGAATAATCTCCTGTTAATATGGTGTACATTTCTCTGA 2017
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QY 2018 TTATTTCTACACATACATGTAATATGCTCTTCTTTTAAATAGGTTGCTACTATGC 2077
Db 6747 TTATTTCTACACATACATGTAATATGCTCTTCTTTTAAATAGGTTGCTACTATGC 6806
QY 2078 TGTATAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAACAGCA 2137
Db 6807 TGTATAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAACAGCA 6866

RESULT 11
G07115 LOCUS human STS WI-9098, sequence tagged site. STS 19-OCT-1995
DEFINITION G07115
ACCESSION G07115.1 GI:860360
VERSION

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

STS: STS sequence; primer; sequence tagged site.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1180)
Hudson.T.
Whitehead Institute/MIT Center for Genome Research; Physically
Mapped ESTs
Unpublished (1995)
Contact: Thomas Hudson
Whitehead Institute/MIT Center for Genome Research
Whitehead Institute for Biomedical Research
9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TCAGGCTTGGAGCAGTAGCT
Primer B: TTGCCGTTGGAGACTCAG
STS size: 125
PCR Profile:
Presoak:
Denaturation:
Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
Protocol:
Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 mM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul

Buffer:
MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
pH: 9.3

Prepared with primer pairs derived from M12824 -- Unigene.

FEATURES
Location/Qualifiers
1..1180
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="713_E_9; 774_F_9; 855_H_7; 842_A_10; 937_B_12;
(893-900)_C_12"
STS
primer_bind
395..519
primer_bind
395..414
complement(501..519)
ORIGIN

Query Match 51.5%; Score 1164.2; DB 7; Length 1180;
Best Local Similarity 98.8%; Pred. No. 6.5e-299;
Matches 1166; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 828 CCTGTGCAACGACCACTACATTACTTCAAACTGAGATCCTTCTTTTGGAGGAGCAAGT 887
Db 1 CCTGTGCAACGACCACTACATTACTTCAAACTGAGATCCTTCTTTTGGAGGAGCAAGT 60
QY 888 CCTTCCCTTTTCAATTTTTCAGTCTTCTCCCTGATGATTCATTCATGATTATTTT 947
Db 61 CCTTCCCTTTTCAATTTTTCAGTCTTCTCCCTGATGATTCATTCATGATTATTTT 120
QY 948 TAGTGGGGCGGGGGGAAAGATTACTTTTTTTTATGTGTTTGCACGGGAAACAAACT 1007
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QY 1008 AGGTAAATCTACAGTACACCAAGGGTCAATACTGTTGTGGGCACATCGCGTAGG 1067

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Db 181 AGGTAAATCTACAGTACACCAAGGCTCAAACTACTGTTGTGCGCACATCGCGGTAGG 240
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Qy 1068 GCGTGGAAAGGGCAGGCCAGAGCTACCGCAGAGTTCTCAGAATCTAGTCTGAGAGAGCT 1127
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Db 241 GCGTGGAAAGGGCAGGCCAGAGCTACCGCAGAGTTCTCAGAATCTAGTCTGAGAGAGCT 300
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Qy 1128 GGAGGCACCATGCCATCTCAACCTCTTCCCGCCCGTCTTCAAGAGGGGAGGCTAAAG 1187
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Db 301 GGAGGCACCATGCCATCTCAACCTCTTCCCGCCCGTCTTCAAGAGGGGAGGCTAAAG 360
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Qy 1188 CCCAGAGACGCTTGATCAAGAGGCACACAGCAAGTCAGGTTGGAGCAGTAGTCTGAGGG 1247
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Db 361 CCCAGAGACGCTTGATCAAGAGGCACACAGCAAGTCAGGTTGGAGCAGTAGTCTGAGGG 420
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Qy 1248 ACCTTGCTCCAGCTCAGGGCTCTTCTCCACACCAATTCAGGTCCTTCTTCCGAGGC 1307
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Db 421 ACCTTGCTCCAGCTCAGGGCTCTTCTCCACACCAATTCAGGTCCTTCTTCCGAGGC 480
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Qy 1368 CTTGGGATATCTGTGCCAGAGCCTCGAGGAGTAAATGAATTAAGAGAGAACTGCCTTT 1427
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Qy 1428 GGCAGAGTTCTAATGTAATGTAATATCAGACTTTTTTTTTTTTAAATCAAGCCTAAAT 1487
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Db 601 GGCAGAGTTCTAATGTAATGTAATATCAGACTTTTTTTTTTTTAAATCAAGCCTAAAT 660
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Qy 1488 TGTATAGACCTAAATAAATGAAGTGTGAGCTTAAACCCCTGGAAATGAATCCCTCTAT 1547
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Qy 1548 CTTAAAGAAATCTCTGTGAAAACCCCTATGTGAGGCGGAATGCTCTCCAGCCCTTG 1607
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Qy 1608 CATTCAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCAT 1667
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Db 781 CATTCAGAGGGCCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCAT 840
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Qy 1668 CAGTGAGTTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTG 1727
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Db 841 CAGTGAGTTAAACTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTG 900
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Qy 1728 GGATCACTGATGACTTTTATCTTTGTAAGACAAATTTGAGAGAGCCCTCACAAGC 1787
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Db 901 GGATCACTGATGACTTTTATCTTTGTAAGACAAATTTGAGAGAGCCCTCACAAGC 960
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Qy 1788 CCTGCCCTCTGCTCAACTAGCAGATACAGGAGTGAAGGACCTGACTCTCTTAAGGAGG 1847
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Db 961 CCTGCCCTCTGCTCAACTAGCAGATACAGGAGTGAAGGACCTGACTCTCTTAAGGAGG 1020
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Qy 1848 CTGAGAGCCCAACTGCTGTCCCAACATGCACTTCTTGTGTTAAGGTATGGTACAAGCA 1907
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Db 1021 CTGAGAGCCCAACTGCTGTCCCAACATGCACTTCTTGTGTTAAGGTATGGTACAAGCA 1080
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Qy 1908 ATGCTGCCCATTGGAGAGAAAACCTTAAGTAGTAAGGAAATTAAGAACCACTATAAT 1967
|||||
Db 1081 ATGCTGCCCATTGGAGAGAAAACCTTAAGTAGTAAGGAAATTAAGAACCACTATAAT 1140
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Qy 1968 TCTTCACTTAGGAATAATCTCTGTTAATATGGGTGACA 2007
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Db 1141 TCTTCACTTAGGAATAATCTCTGTTAATATGGGTGACA 1180

RESULT 12
LOCUS CQ725925 1059 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 11859 from Patent WO20069579.
ACCESSION CQ725925

VERSION CQ725925.1 GI:42287423
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 11859 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1. 1059
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 46.8%; Score 1059; DB 2; Length 1059;
Best Local Similarity 100.0%; Pred. No. 6.6e-271;
Matches 1059; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 56 CGGTCCCGCGCGCTCCCTCGCGCGAGCTTCGAGCCAAAGCAGCTCTCTGGGAGCG 115
Db 1 CGGCTCCCGCGCGCTCCCTCGCGCGAGCTTCGAGCCAAAGCAGCTCTCTGGGAGCG 60
Qy 116 CGTCATGGCCTTACAGTGACCGGCTTGCTCTCGCGCTGGCCTTGCTGCCACGCCG 175
Db 61 CGTCATGGCCTTACAGTGACCGGCTTGCTCTCGCGCTGGCCTTGCTGCCACGCCG 120
Qy 176 CAGCCGAGCAGGCTTCGCGGTGTGCGGCTCGATCGGACCTCGGAACCTTGGGCGAGACAGT 235
Db 121 CAGCCGAGCAGGCTTCGCGGTGTGCGGCTCGATCGGACCTTGGAACTTGGGCGAGACAGT 180
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Db 181 GGAGCTGAAGTGCAGAGTGTGCTGTCCAAACCCGAGCGTGGGCTGCTCGTGGCTTTCCA 240
Qy 296 GCGCGCGCGCGCGCGCGCGCTTCCACTTCTCTATACCTCTCCCAAAACAGCCCAA 355
Db 241 GCGCGCGCGCGCGCGCGCGCTTCCACTTCTCTATACCTCTCCCAAAACAGCCCAA 300
Qy 356 GCGCGCGCGCGCGCTTGAGACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGT 415
Db 301 GCGCGCGCGAGGGGCTGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGT 360
Qy 416 CCTCACTGAGCGACTTTCGCGCGAGAGAAAGAGGGCTACTATTTCTGCTCGGCCCTGAG 475
Db 361 CCTCACTGAGCGACTTTCGCGCGAGAGAAAGAGGGCTACTATTTCTGCTCGGCCCTGAG 420
Qy 476 CAATCTCATGCTACTTTCAGCCACTTGTGCGCGGTCTTCTGCGCAGCGAGAGCCACAC 535
Db 421 CAATCTCATGCTACTTTCAGCCACTTGTGCGCGGTCTTCTGCGCAGCGAGAGCCACAC 480
Qy 536 GACGCGCAGCGCGCGAGCCACCAACACCGCGCGCCACCATCGCGTCGCGAGCCCTGTGCC 595
Db 481 GACGCGCAGCGCGCGAGCCACCAACACCGCGCGCCACCATCGCGTCGCGAGCCCTGTGCC 540
Qy 596 GCGCCAGAGCGGTGCGCGCGCAGCGCGGGGGCGCAGTGCACACGAGGGGGCTGGAATT 655
Db 541 GCGCCAGAGCGGTGCGCGCGCAGCGCGGGGGCGCAGTGCACACGAGGGGGCTGGAATT 600
Qy 656 GCGCTGTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTC 715
Db 601 GCGCTGTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTC 660
Qy 716 ACTGTTATCACCTTTTACTGCAACCAAGGAAACGAAAGACGTTGTTTGCAAATGTCCTCG 775
Db 661 ACTGTTATCACCTTTTACTGCAACCAAGGAAACGAAAGACGTTGTTTGCAAATGTCCTCG 720

QY 776 GCCTGTGTCATAATCGGAGACAAGCCCGAGCCCTTCGGCGAGATACGCTAAACCCCTGTGC 835
 Db 721 GCCTGTGTCATAATCGGAGACAAGCCCGAGCCCTTCGGCGAGATACGCTAAACCCCTGTGC 780
 QY 836 AACAGCCACTACATTAATCTCAAACTCAGATCCCTTCCTTTGAGGAGCAAGTCCTTCCTT 895
 Db 781 AACAGCCACTACATTAATCTCAAACTCAGATCCCTTCCTTTGAGGAGCAAGTCCTTCCTT 840
 QY 896 TTCATTTTTCAGTCTTCTCCCTCGTGTATTCATCTCATGATTTATTTTAGTGGGG 955
 Db 841 TTCATTTTTCAGTCTTCTCCCTCGTGTATTCATCTCATGATTTATTTTAGTGGGG 900
 QY 956 GCGGGTGGGAAGATTACTTTTCTTTATGTGTTGACGGGAAACAACTAGGTAA 1015
 Db 901 GCGGGTGGGAAGATTACTTTTCTTTATGTGTTGACGGGAAACAACTAGGTAA 960
 QY 1016 TCTACAGTACACCAAGGTCACATCTGTTGTGCGCACATCGCGTAGGCGTGGAA 1075
 Db 961 TCTACAGTACACCAAGGTCACATCTGTTGTGCGCACATCGCGTAGGCGTGGAA 1020
 QY 1076 AGGGCAGCCGACGAGTACCCGACAGATCTCTCAGATCA 1114
 Db 1021 AGGGCAGCCGACGAGTACCCGACAGATCTCTCAGATCA 1059

RESULT 13

AC169881/c

LOCUS

DEFINITION Macaca mulatta clone CH250-110A2, *** SEQUENCING IN PROGRESS ***,
 20 unordered pieces.

AC169881

AC169881.1 GI:77539568

HTG; HTGS PHASE1.

SOURCE Macaca mulatta (chesus monkey)

ORGANISM

Macaca mulatta

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

1 (bases 1 to 72869)

Muzny D.M., Abraham K.K., Abulimiti, A., Adams, C.Q., Aduba, G.,

Allen, C.C., Alsbrooks, S.L., Anosike, U.S., Archer, P.M.,

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Hitchens, M.E., Hodgson, A.V., Hogue, M.E., Holder, M., Hollins, B.,

Howell, L.L., Huijck, S.W., Hume, J., Jackson, A., Jackson, L.R.,

Joshi, V., Joy, C., Kalkai, F.B., Kalafus, K.J., Kalu, J.B., Kang, Y.,

Koeber, J., Khan, Z.M., Kidwai, S., King, L.M., Kisamo, H., Kovar, C.L.,

Kwila, A.N., Kwis, C.R., Lago, L.A., Lago, M.T., Lai, C., Lara, F.,

Le, T.T., Lee, S.L., Lee, T.W., Legall, iii, F.H., Lemon, S.J.,

Lewis, L.R., Li, B., Li, Y., Li, Z., Linnell, M.A., Liu, J., Liu, W.,

Liu, Y., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhera, L.M.,

Lozano, R.J., Luc, T., Madu, R.C., Maheshwari, M., Maheshwari, R.,

Malloy, K., Mansouri, D.L., Martinez, E., Matejkova, P., Mathew, T.,

McCauley, S.K., McPherson, J.D., Mercado, C., Mercado, I.C.,

Metzker, M.B., Millin, A., Milosavljevic, A., Morgan, M.B., Morris, S.,

Munidaa, M., Murray, D.D., Muzny, D.M., Nazareth, L.V., Ngo, D.N.,

Nguyen, H.T., Nguyen, N.B., Nguyen, P.Q., Nwaokelimeh, O.O.,

Obregon, M., Odeh, E.A., Okonkwo, F., Okwuonu, G.O., Okwuonu, K.C.,
 Onyenekwe, J., Parish, B.J., Parker, D.N., Parra, A.A., Pasternak, S.,
 Patel, B.M., Patel, R.R., Paul, H.A., Perez, A., Perez, L.M., Puazo, M.,
 Perz, Y., Pham, T.L., Player, E.J., Primus, E.L., Pu, L., Puazo, M.,
 Purkiss, C., Qin, X., Quiroz, J.B., Rabata, D., Rachlin, E.K., Ren, Y.,
 Richards, S., Rojas, A., Ruiz, S., Sabo, A., Santibanez, J.,
 Savary, G.G., Scherer, S.E., Schneider, B.W., Sebasigari, R.,
 Sexton, M.M., Shen, H., Shen, Y., Sisson, I., Sneed, A.J., Sodergren, E.,
 Song, X., Sorelle, R.P., Svatek, A.F., Taylor, E.W., Taylor, T.R.,
 Thelus, R., Thomas, N., Thorn, R.D., Thornton, R.D., Tong, M.Y.,
 Trejos, Z.Y., Usmani, K., Vargo, C.E., Vattathil, S., Vega, R.A.,
 Villanueva, D., Volkov, A., Walker, D.L., Wang, Q., Wang, S.,
 Warren, J.T., Watt, J.E., Wei, X., Wheeler, D.A., White, C.S., Williams
 Jr, R.L., Williams, A.C., Williams, G.A., Williams, J.D., Wilson, K.,
 Woodworth, J.R., Worley, K.C., Wright, R.A., Wu, J., Wu, W., Yakub, S.,
 Yerrapragada, S., Yu, F., Yuan, D.T., Yuan, Y., Zhang, J., Zhang, L.,
 Zhang, Z., Zhou, J., Zhu, Y., Weinstock, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

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Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

----- Project Information

Center project name: LBOOK

Center clone name: CH250-110A2

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 83719 bases at least Q40

Consensus quality: 87952 bases at least Q30

Consensus quality: 90578 bases at least Q20

Estimated insert size: 97635; sum-of-contigs estimation

Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 20 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 4184: contig of 4184 bp in length

* 4185: gap of unknown length

* 4285: contig of 2432 bp in length

* 6717: gap of unknown length

* 6817: contig of 2739 bp in length

* 9556: gap of unknown length

* 9656: contig of 2485 bp in length

* 12141: contig of 2485 bp in length

* 12240: gap of unknown length

* 14405: contig of 2165 bp in length

* 14505: gap of unknown length

* 14506: contig of 5162 bp in length

* 19668: gap of unknown length

* 19767: contig of 3536 bp in length

* 23303: contig of 3536 bp in length

* 23404: gap of unknown length

* 25996: contig of 2593 bp in length

* 25997: gap of unknown length

* 28972: contig of 2876 bp in length

* 28973: gap of unknown length

* 35138: contig of 6066 bp in length

* 35238: gap of unknown length

| | | | | | |
|---|-------|--------|--------|------------|--------------|
| * | 35239 | 37258: | contig | of 2020 | bp in length |
| * | 37359 | 37358: | gap | of unknown | length |
| * | 37359 | 40624: | contig | of 3266 | bp in length |
| * | 40624 | 40624: | gap | of unknown | length |
| * | 40625 | 40724: | gap | of unknown | length |
| * | 40725 | 45983: | contig | of 5259 | bp in length |
| * | 45984 | 46083: | gap | of unknown | length |
| * | 46084 | 48189: | contig | of 2106 | bp in length |
| * | 48190 | 48189: | gap | of unknown | length |
| * | 48290 | 51710: | contig | of 3421 | bp in length |
| * | 51711 | 51810: | gap | of unknown | length |
| * | 51811 | 56840: | contig | of 5030 | bp in length |
| * | 56841 | 56940: | gap | of unknown | length |
| * | 56941 | 59702: | contig | of 2762 | bp in length |
| * | 59703 | 59802: | gap | of unknown | length |
| * | 59803 | 63695: | contig | of 3893 | bp in length |
| * | 63696 | 63795: | gap | of unknown | length |
| * | 63796 | 68927: | contig | of 5132 | bp in length |
| * | 68928 | 69027: | gap | of unknown | length |
| * | 69028 | 72869: | contig | of 3842 | bp in length |

| ORIGIN | / estimated_length unknown | | | | | | | | | |
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| Query Match | 46.8% | Score 1053; | DB 12; | Length 72869; | | | | | | |
| Best Local Similarity | 85.4%; | Pred. No. 2.4e-269; | | | | | | | | |
| Matches 1266; | Conservative 0; | Mismatches 110; | Indels 107; | Gaps 4; | | | | | | |
| Qy 759 | GTTTGCAAAATGTC | CCCGGCCTGTGGTCAAA | TGGGAGACAAGCCAGC | CTTTTCGGCGAGA | 818 | | | | | |
| Db 19383 | GCCTTCCTCTTCTTCA | GGCCCTGTGGTCAAA | TGGGAGGCAAGCCAGC | CTTTTCGACAGA | 19324 | | | | | |

| | | | |
|----|-------|--|-------|
| Qy | 819 | TAGCTCTAAACCTGTGCGAAACGCCACTACATTACTTTCAAACGTGAGATCCTTCCTTTTGAG | 878 |
| Db | 19323 | TAGCTCTAAACCTGTGCGCAACGCCACTAGCTTACTTTCAAACGTGAGATCCTTCCTTTTGAG | 19264 |
| Qy | 879 | GGAGCAAGTCCTTTCCCTTTTCATTTTTTCCAGCTCTTCCTCCCTGTGTATTCATTCTCATGA | 938 |
| Db | 19263 | GGAGCAAGTCCTTTCCCTTTTGTTTTTTCAGTCTTTCCCTCCCTAUGTATTCATTCTCATGA | 19204 |
| Qy | 939 | TTATTATTTTAGTGGGGCGGGTGGGAAAGATTACTTTTCTTTATGTGTTTGACGGGA | 998 |
| Db | 19203 | TTATTCTGTTTAGTGGGGTGGGGTGGGAAAGATTACTTTTCTTTATGTGTTTGACGGGA | 19144 |
| Qy | 999 | AACAAACTAGGTAAAACTCTACAGTACACCAAGGGTCAAACTACTCTGTGGCGCACAT | 1058 |
| Db | 19143 | AACAAACTAGGTAAAACTCTACAGTACACCGAAGGGTCAAACTACTCTGTGTGCACACAT | 19084 |
| Qy | 1059 | CGCGGTAGGCGGTGGAAGGGGCGAGCCAGAGCTACCGCGAGAGTTCTCAGAATCATGCT | 1118 |
| Db | 19083 | CGGGGTAGGCTGTGGAAAGGGGCAAGTCGGAGCTACCCGCGAGAGTTCTCAGAACTCATGCT | 19024 |
| Qy | 1119 | GAGAGAGCTGGAGGCAACCATGCCATCTCAACCTCTTCCCGCCCGTTTTTACAAGGGGG | 1178 |
| Db | 19023 | GACAGAGCTGGAGGCAACCTGTGCTATCTCAACCTCTTCCCAACCCATTTTACAAGGGGG | 18964 |
| Qy | 1179 | AGGCTAAAGCCACAGACAGCTTTGATCAAAGGCAACACAGCAAGTCAGAGTTGGAGCAGTA | 1238 |
| Db | 18963 | AGGCTAAAGCCACAGACAGCTTTGATCAAAGGCAACACAGCAAGTCAGAGTTGGAGCAGTA | 18904 |
| Qy | 1239 | GCTGGAGGACCTTGTCTCCAGCTCAGGGCTCTTTCTCTCACACCATTCAGGTCCTTTCT | 1298 |
| Db | 18903 | GCTGGAGGACCTTATCTCCAGCTCAGGGCTCTTTCTCTCACACCATTCAGGTCCTTTCT | 18844 |
| Qy | 1299 | TTCCGAGGGCCCTGTCTCAGGGTGAGGTGCTTGAGTCTCCACGCAAGGGAACAAGTAC | 1358 |
| Db | 18843 | TTCCAGAGGACCTGTCTCAGGGCGAGTTCGTTGAGTCTCCAACTCGAAGGGAACAAGTAC | 18784 |
| Qy | 1359 | TTCTTGATACCTGGGATACTGTGCCAGAGCCTCGAGGAGGTAAATGAAT-----AAAGAA | 1414 |
| Db | 18783 | TTCTTGATACCTGGGATAATTGTGCCAGAGTCTCGAGGAGGTAAATGAATCTCGCCTTTGG | 18724 |
| Qy | 1415 | GAGAACTGCCCTTTGGCAGAGTTCATATATGTAAC----- | 1449 |
| Db | 18723 | CAGAGTTATATATATGATATAGTTATATATATGTAACCATCAGAGCTCTTTTAAATATAATCAA | 18664 |
| Qy | 1450 | ----- | 1449 |
| Db | 18663 | GTCTAAATTCGTAGACCTAAATATAAATGAAGGGTGAGCTTAACCCCTGAAATCTAT | 18604 |
| Qy | 1450 | -----AATATCAGACT-TTTTTTTTTTTATAATCAAGCCTAAAAATGTTATAG | 1494 |
| Db | 18603 | AGTTATATAATGTAAACATCAGACTCTTTTTTTTATAATAATCAAGTCTAAATTTCTGTAG | 18544 |
| Qy | 1495 | ACCTAAATAATAATGAAGTGGTGAGCTTAACCCCTGGAAAAATCAATCCCTCTATCTCTAAA | 1554 |
| Db | 18543 | ACCTAAATAATAATGAAGCGGTGAGCTTAACCCCTGAAATCTTAATCCCTCTCTCTGTAAA | 18484 |
| Qy | 1555 | GAAAACTCTGTGAAAACCCCTATGTGGAGCGGAATTGCTCTCCAGCCCTTGCATTGCA | 1614 |
| Db | 18483 | GAAAACTCTGTGAAAACCTGTACATGGTTTCAGAAATGCTCTCCAGCCCTTGCATTGCA | 18424 |
| Qy | 1615 | GAGGGGCCATGAAAGAGCAGGCTACCCCTTTACAAATAGAAATTTGAGCATCATGTAG | 1674 |
| Db | 18423 | GAGGGGCCGTGAAAGAGGAGGCGCACCTCTTTTACAAATAGAAATTTGAGCATCATGTAG | 18364 |
| Qy | 1675 | GTTAAACTAAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTTCTTGGGATCAC | 1734 |
| Db | 18363 | GTTAAACTAAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGCTCCTGGGATCAC | 18304 |
| Qy | 1735 | TGATGACTTTTATATCTTTGTGTAAAGCAATTTGTTGGAGGCCCTCTCACAGCCCTGGCC | 1794 |
| Db | 18303 | TGATGACTTTTATATCTTTGTCAAGACAAATTTGTTGGAGGCCGTCTCGCACGCCCTGGCC | 18244 |
| Qy | 1795 | TCGTCTCAACTAGCAGATACAGGATGAGGCGAGACTGACTCTCTTTAAGGAGGCTGAGAG | 1854 |

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|----------------------------|--|--|------------------------|
| Db | 18243 | TCTGCTCAACTAGCAGATACGGGGATGAGCGACCTGACTCTCTTTAAGGAGCTGAGAG | 18184 |
| Qy | 1855 | CCCAAACTGCTGCTCCCAAAATGCACTTCTCTTCTTAAGATATGGTATGATCAAGCAATGCTTG | 1914 |
| Db | 18183 | CCCAAACTGCTGCTCCCAAAACGCGCTTCTTGCATACAGTATGGTACAGCAATGCTTG | 18124 |
| Qy | 1915 | CCCATTTGGAGAGAAAACCTTAAGTAGATAGAAATAGAACCACTCATATAATCTTTAC | 1974 |
| Db | 18123 | CCCATTTGGAGAGAAAACCTTAAGTAGATAGAAATAGAACCACTCATATAATCTTTAC | 18064 |
| Qy | 1975 | CTTAGGAATAATCTCTGTTAATATGCTGATCTTCTCTCTGATTTATTTCTTACACATAC | 2034 |
| Db | 18063 | CTTAGGAATAATCTCTGTTAATATGCTGATCTTCTCTCTGATTTATTTCTTACATAC | 18007 |
| Qy | 2035 | ATGTAATAATGATCTTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTA | 2094 |
| Db | 18006 | GTGTAATAATGATCTTTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTA | 17947 |
| Qy | 2095 | ATGAATAAATCTTTAGCATCTCTTTTAAATAGGGTTAAACAGCA | 2137 |
| Db | 17946 | ATGAATAAATCTTTAGCATCTCTTTTAAATAGGGTTAAACAGCA | 17904 |
| RESULT 14 | | | |
| LOCUS | I23895 | Sequence 11 from patent US 5540926. | linear PAT 07-OCT-1996 |
| DEFINITION | I23895 | Sequence 11 from patent US 5540926. | |
| ACCESSION | I23895 | | |
| VERSION | I23895.1 | GI:1603765 | |
| KEYWORDS | Unknown. | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 1060) | | |
| AUTHORS | Aruffo, A., Hollenbaugh, D. and Ledbetter, J. A. | | |
| TITLE | Soluble and its use in B cell stimulation | | |
| JOURNAL | Patent: US 5540926-A 11 30-JUL-1996; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..1060 | | |
| | /organism="unknown" | | |
| | /mol_type="unassigned DNA" | | |
| ORIGIN | | | |
| Query Match | 46.4%; | Score 1048; DB 2; Length 1060; | |
| Best Local Similarity | 100.0%; | Pred. No. 5.6e-268; | |
| Matches 1048; Conservative | 0; Mismatches | 0; Indels | 0; Gaps 0; |
| Qy | 67 | CGCCTCCCTCGCGCCGAGCTTCGAGCCAGCAGCGTCTCTGGGAGCGCGTCATGGCCT | 126 |
| Db | 13 | CGCCTCCCTCGCGCCGAGCTTCGAGCCAGCAGCGTCTCTGGGAGCGCGTCATGGCCT | 72 |
| Qy | 127 | TACCACTGACCGCTTGTCTCTGCGCGTGGCTGCTGCTCCACCGCGCAGCGCGAGCC | 186 |
| Db | 73 | TACCACTGACCGCTTGTCTCTGCGCGTGGCTGCTGCTCCACCGCGCAGCGCGAGCC | 132 |
| Qy | 187 | AGTTCGGGTGTGCGCGCTGGATCGGACTGGAACCTGGCGAGACAGTGGAGCTGAAGT | 246 |
| Db | 133 | AGTTCGGGTGTGCGCGCTGGATCGGACTGGAACCTGGCGAGACAGTGGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGTGTGCTGTCCAAACCGAGCTCGGCTGCTCGTGGCTCTTCCAGCCGCGCGGG | 306 |
| Db | 193 | GCCAGTGTGCTGTCCAAACCGAGCTCGGCTGCTCGTGGCTCTTCCAGCCGCGCGGG | 252 |
| Qy | 307 | CGCCCGCAGTCCCACTTCTCTTACCTCTCCCAAAACAGCCCAAGCGCGCGCGAGG | 366 |
| Db | 253 | CGCCCGCAGTCCCACTTCTCTTACCTCTCCCAAAACAGCCCAAGCGCGCGCGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGTTCGGGACACCTTGTCTCTCACCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGTTCGGGACACCTTGTCTCTCACCTGA | 372 |
| Qy | 427 | CGGACTTCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCA | 486 |

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|----------------------------|---|--|------------------------|
| Db | 373 | GGGACTTCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCA | 432 |
| Qy | 487 | TGTACTTTAGCCACACTTCTGTCGCGTCTTCTCTCCAGCGAAGCCACACGAGCGCAGCGC | 546 |
| Db | 433 | TGTACTTTAGCCACACTTCTGTCGCGTCTTCTCTCCAGCGAAGCCACACGAGCGCAGCGC | 492 |
| Qy | 547 | CCGCAACCAACACACCGGCGCCACCATCGCGTCGCGAGCCCTGTCCCTGCGGCCAGAGG | 606 |
| Db | 493 | CCGCAACCAACACACCGGCGCCACCATCGCGTCGCGAGCCCTGTCCCTGCGGCCAGAGG | 552 |
| Qy | 607 | CGTGGCGGCGAGCGGCGGCGGCGAGTCACACGAGGGGCTGGAATTGCGCTGTGATA | 666 |
| Db | 553 | CGTGGCGGCGAGCGGCGGCGGCGAGTCACACGAGGGGCTGGAATTGCGCTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGGCGCCCTTGGCGGCGGACTTGTGGGCTCTCTCTCTGCTCACTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGGCGGCGCCCTTGGCGGCGGACTTGTGGGCTCTCTCTCTGCTCACTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACCAACGAGAACCGAAGACGTTTTCGCAAAATGTCTCCCGCCCTGTGCTCA | 786 |
| Db | 673 | CCCTTTACTGCAACCAACGAGAACCGAAGACGTTTTCGCAAAATGTCTCCCGCCCTGTGCTCA | 732 |
| Qy | 787 | AATCGGAGACAAGCCCGAGCCCTTTCGCGGAGATAGCTCTAAACCTGTGTGCAACGACACTA | 846 |
| Db | 733 | AATCGGAGACAAGCCCGAGCCCTTTCGCGGAGATAGCTCTAAACCTGTGTGCAACGACACTA | 792 |
| Qy | 847 | CATTACTTCAAACTCAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTCAATTTTTC | 906 |
| Db | 793 | CATTACTTCAAACTCAGATCTCTCTTTTGGAGGAGCAAGTCTCTCCCTTCAATTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCCTCTGTATTCAATCTCATGATTAATTTTAGTGGGCGCGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCCTCTGTATTCAATCTCATGATTAATTTTAGTGGGCGCGGGTGGGA | 912 |
| Qy | 967 | AAGATTACTTTTCTTTATGTTTTCGCGGAAACAAAACCTAGGTAAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTACTTTTCTTTATGTTTTCGCGGAAACAAAACCTAGGTAAATCTACAGTACA | 972 |
| Qy | 1027 | CCACAAGGCTCAATACTGTTTGTGGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC | 1086 |
| Db | 973 | CCACAAGGCTCAATACTGTTTGTGGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC | 1032 |
| Qy | 1087 | AGAGCTACCCGAGAGTCTCTCAGAACTCA | 1114 |
| Db | 1033 | AGAGCTACCCGAGAGTCTCTCAGAACTCA | 1060 |
| RESULT 15 | | | |
| LOCUS | AR380469 | Sequence 1014 from patent US 6607879. | linear PAT 18-DEC-2003 |
| DEFINITION | AR380469 | Sequence 1014 from patent US 6607879. | |
| ACCESSION | AR380469 | | |
| VERSION | AR380469.1 | GI:40088103 | |
| KEYWORDS | Unknown. | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 1060) | | |
| AUTHORS | Cocks, B.G., Stuart, S.G. and Seilhamer, J.J. | | |
| TITLE | Compositions for the detection of blood cell and immunological response gene expression | | |
| JOURNAL | Patent: US 6607879-A 1014 19-AUG-2003; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..1060 | | |
| | /organism="unknown" | | |
| | /mol_type="genomic DNA" | | |
| ORIGIN | | | |
| Query Match | 46.4%; | Score 1048; DB 2; Length 1060; | |
| Best Local Similarity | 100.0%; | Pred. No. 5.6e-268; | |
| Matches 1048; Conservative | 0; Mismatches | 0; Indels | 0; Gaps 0; |

Search completed: May 30, 2006, 09:01:49
Job time : 12409 secs

| | | | |
|----|------|---|------|
| Qy | 67 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCTGCGGAGCGCGTCATGCGCT | 126 |
| Db | 13 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCTGCGGAGCGCGTCATGCGCT | 72 |
| Qy | 127 | TACAGTGACCGCTTGCCTCGCGCTGCGCTTGCCTCCACGCGCCAGCGCGGAGCC | 186 |
| Db | 73 | TACAGTGACCGCTTGCCTCGCGCTGCGCTTGCCTCCACGCGCCAGCGCGGAGCC | 132 |
| Qy | 187 | AGTTCCGGGTGTCGCGCTGCGCTTGCCTCCGAACTGGCGGAGACAGTGAGCTGAAGT | 246 |
| Db | 133 | AGTTCCGGGTGTCGCGCTGCGCTTGCCTCCGAACTGGCGGAGACAGTGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGTGCTGCTGTCCAAACCGCAGTCGCGCTGCTGCTGCTTCCAGCGCGCGGCG | 306 |
| Db | 193 | GCCAGTGCTGCTGTCCAAACCGCAGTCGCGCTGCTGCTGCTTCCAGCGCGCGGCG | 252 |
| Qy | 307 | CCGCGCCAGTCCACACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGCGCGAGG | 366 |
| Db | 253 | CCGCGCCAGTCCACACCTTCTCTATACCTCTCCCAAAACAAGCGCGCGCGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTCTCGGCGCAAGAGGTTGGGGGACACCTTCTCACCCCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTCTCGGCGCAAGAGGTTGGGGGACACCTTCTCACCCCTGA | 372 |
| Qy | 427 | GCGACTTCCGCGGAGAGAAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAACTCCATCA | 486 |
| Db | 373 | GCGACTTCCGCGGAGAGAAACGAGGGCTACTATTTCTGCTCGGCGCTGAGCAACTCCATCA | 432 |
| Qy | 487 | TGTACTTCAGCACTTCGTCGCGGTCTTCTCCAGCGCAAGCCCAACGAGCGCGAGCGC | 546 |
| Db | 433 | TGTACTTCAGCACTTCGTCGCGGTCTTCTCCAGCGCAAGCCCAACGAGCGCGAGCGC | 492 |
| Qy | 547 | CGGACACCAACACCGCGCGCCACATCGCGTTCGAGCGCTGTCCTCGCGCCAGAGG | 606 |
| Db | 493 | CGGACACCAACACCGCGCGCCACATCGCGTTCGAGCGCTGTCCTCGCGCCAGAGG | 552 |
| Qy | 607 | CGTGC CGGCCAGCGCGCGGGCGCGAGTGCAACGAGGGGCTGGAATTCCGCTGTGATA | 666 |
| Db | 553 | CGTGC CGGCCAGCGCGCGGGCGCGAGTGCAACGAGGGGCTGGAATTCCGCTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGCGCCCTTGGCGGGACTTGTGGGTCCTTCTCTGTCACCTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGCGCCCTTGGCGGGACTTGTGGGTCCTTCTCTGTCACCTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACCAACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGGCTGTGTCA | 786 |
| Db | 673 | CCCTTTACTGCAACCAACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGGCTGTGTCA | 732 |
| Qy | 787 | AATCGGAGACAAGCCAGCCCTTTCGCGGAGATAGCTCTAACCTGTGTGCAACAGCCACTA | 846 |
| Db | 733 | AATCGGAGACAAGCCAGCCCTTTCGCGGAGATAGCTCTAACCTGTGTGCAACAGCCACTA | 792 |
| Qy | 847 | CATTACTTCAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCCCTTTCATTTTTTC | 906 |
| Db | 793 | CATTACTTCAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCCCTTTCATTTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTAGTGGGGGGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTAGTGGGGGGGGTGGGA | 912 |
| Qy | 967 | AAGATTAATTTTCTTTATGTTTGGCGGGAACAAAACTAGGTAAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTAATTTTCTTTATGTTTGGCGGGAACAAAACTAGGTAAATCTACAGTACA | 972 |
| Qy | 1027 | CCACAAGGTCACATACCTTGTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC | 1086 |
| Db | 973 | CCACAAGGTCACATACCTTGTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC | 1032 |
| Qy | 1087 | AGAGTACCCCGAGAGTTCTCAGAATCA | 1114 |
| Db | 1033 | AGAGTACCCCGAGAGTTCTCAGAATCA | 1060 |

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 29, 2006, 21:45:26 ; Search time 2523 Seconds
(without alignments)
6248.218 Million cell updates/sec
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Total number of hits satisfying chosen parameters: 10489840
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15: Geneseqn2006s.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | | | | | | | | | |
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| 1 | 2261 | 100.0 | 2261 | 12 | ADP10406 | Reference | Adp10406 | Reference | |
| 2 | 2261 | 100.0 | 2261 | 13 | ADG92791 | Nucleotid | Adg92791 | Nucleotid | |
| 3 | 2261 | 100.0 | 2261 | 13 | ADG19437 | DNA of th | Adg19437 | DNA of th | |
| 4 | 2261 | 100.0 | 2261 | 14 | ADW86779 | Human CD8 | Adw86779 | Human CD8 | |
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| 6 | 2132.8 | 94.3 | 3048 | 12 | ADQ64633 | Novel hum | Adq64633 | Novel hum | |
| 7 | 2061.6 | 91.2 | 2134 | 12 | ADQ22926 | Human sof | Adq22926 | Human sof | |
| 8 | 2061.2 | 91.2 | 2123 | 10 | ADP90782 | Human hep | Adp90782 | Human hep | |
| 9 | 2029 | 89.7 | 2150 | 13 | ADG92793 | CDNA of a | Adg92793 | CDNA of a | |
| 10 | 2029 | 89.7 | 2150 | 13 | ADG19439 | Human sec | Adg19439 | Human sec | |
| 11 | 2029 | 89.7 | 2150 | 14 | ADZ26403 | Human CD8 | Adz26403 | Human CD8 | |
| 12 | 1905 | 84.3 | 3518 | 14 | AED96282 | Human C-r | Aed96282 | Human C-r | |
| 13 | 1821 | 80.5 | 3476 | 14 | AED96284 | Human C-r | Aed96284 | Human C-r | |
| 14 | 1683 | 74.4 | 3407 | 14 | AED96285 | Human C-r | Aed96285 | Human C-r | |
| 15 | 1683 | 74.4 | 3743 | 14 | AED96281 | Human C-r | Aed96281 | Human C-r | |
| 16 | 1393 | 61.6 | 4392 | 14 | AED96283 | Human C-r | Aed96283 | Human C-r | |
| 17 | 1361.4 | 60.2 | 1729 | 12 | ADQ18424 | Human sof | Adq18424 | Human sof | |
| 18 | 1361.4 | 60.2 | 1729 | 13 | ACF87521 | Human SIR | Acf87521 | Human SIR | |

| | | | | | | |
|----|-------|------|------|----|----------|-----------|
| 19 | 1048 | 46.4 | 1060 | 2 | AAQ57986 | Genomic s |
| 20 | 1048 | 46.4 | 1060 | 10 | ADD25612 | Binding d |
| 21 | 1048 | 46.4 | 1060 | 11 | ADI31688 | Human CDN |
| 22 | 1048 | 46.4 | 1060 | 13 | ADS83755 | Human lym |
| 23 | 761.4 | 33.7 | 773 | 3 | AAZ29002 | Human CD8 |
| 24 | 744 | 32.9 | 744 | 14 | AED96294 | Human C-r |
| 25 | 708 | 31.3 | 708 | 2 | AAZ80967 | Human CD8 |
| 26 | 708 | 31.3 | 708 | 8 | ABZ69260 | Human CD8 |
| 27 | 708 | 31.3 | 708 | 13 | ADS92817 | Nucleotid |
| 28 | 708 | 31.3 | 708 | 13 | ADS19462 | Coding se |
| 29 | 708 | 31.3 | 708 | 14 | ADV42461 | Human psy |
| 30 | 708 | 31.3 | 708 | 15 | AEF68357 | Human CD8 |
| 31 | 704.8 | 31.2 | 708 | 8 | ABZ69262 | Human CD8 |
| 32 | 676 | 29.9 | 727 | 10 | ADF90668 | Human hep |
| 33 | 646.4 | 28.6 | 662 | 12 | ADN11772 | Human CD8 |
| 34 | 644.4 | 28.5 | 1637 | 12 | ADN11778 | Human CD8 |
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| 36 | 610.4 | 27.0 | 708 | 13 | ADS92815 | Nucleotid |
| 37 | 610.4 | 27.0 | 708 | 13 | ADS19461 | DNA of th |
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| 39 | 593 | 26.2 | 610 | 13 | ADU12274 | Solid tum |
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| 41 | 557.4 | 24.7 | 2001 | 13 | ADS92807 | Nucleotid |
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| 44 | 552 | 24.4 | 1891 | 13 | ADS19455 | DNA of th |
| 45 | 543 | 24.0 | 1131 | 3 | AAZ46253 | CDNA enco |

ALIGNMENTS

RESULT 1
ADP10406
ID ADP10406 standard; DNA; 2261 BP.
XX
AC ADP10406;
XX
DT 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequences for marker probe #83.
XX
KW transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
WPI; 2004-400724/37.
XX
PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
the genes.
XX
PS Claim 80; SEQ ID NO 415; 1762pp; English.
XX
CC The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The

from plasmid only
seq
note
finger

CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
CC and monitoring of allograft rejection and other disorders.
XX
SQ

Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 12; Length 2261;

Best Local Similarity 100.0%; Pred. No. 1.8e-308;

Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1 | GAATCAGCTCCGGGCGCGGGAAGGGCGCAACTTTCCCGCTCGGCGCCCCACCGGCT | 60 |
| Db | 1 | GAATCAGGCTCCGGGCGCGGGAAGGGCGCAACTTTCCCGCTCGGCGCCCCACCGGCT | 60 |
| Qy | 61 | CCGCGCGCCCTCCCTCGCGCGCGAGCTTCGAGCCAAAGAGCTCTCGGGAGCGCGTCA | 120 |
| Db | 61 | CCGCGCGCCCTCCCTCGCGCGCGAGCTTCGAGCCAAAGAGCTCTCGGGAGCGCGTCA | 120 |
| Qy | 121 | TGGCCTTACCAAGTGAACCGCTTGCTTCCTGCGCTGGCTTGCTGCCACGCCCGCAGGC | 180 |
| Db | 121 | TGGCCTTACCAAGTGAACCGCTTGCTTCCTGCGCTGGCTTGCTGCCACGCCCGCAGGC | 180 |
| Qy | 181 | CGAGCAGTTCGGGTGTGCGGCTGGATCGGACCTGGAACTGGGGAGACAGTGGAGC | 240 |
| Db | 181 | CGAGCAGTTCGGGTGTGCGGCTGGATCGGACCTGGAACTGGGGAGACAGTGGAGC | 240 |
| Qy | 241 | TGAAGTGCAGGTGTGCTGTCCAAACCGAGTGGGGTGTCTCGTGGCTCTTCAGCGCG | 300 |
| Db | 241 | TGAAGTGCAGGTGTGCTGTCCAAACCGAGTGGGGTGTCTCGTGGCTCTTCAGCGCG | 300 |
| Qy | 301 | CGCGCGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAAGGCCCAAGGCGG | 360 |
| Db | 301 | CGCGCGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAAGGCCCAAGGCGG | 360 |
| Qy | 361 | CGAGGGCTGGACACCGAGGGTCTCGGGCAAGAGTGGGGAGACCTTCGTCCTCA | 420 |
| Db | 361 | CGAGGGCTGGACACCGAGGGTCTCGGGCAAGAGTGGGGAGACCTTCGTCCTCA | 420 |
| Qy | 421 | CCCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTGCTCGGCCCTGAGCAACT | 480 |
| Db | 421 | CCCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTGCTCGGCCCTGAGCAACT | 480 |
| Qy | 481 | CCATCATGTACTTACGCCACTTCGTGCGGGTCTTCTGCGAGCGAAGCCACCGACGC | 540 |
| Db | 481 | CCATCATGTACTTACGCCACTTCGTGCGGGTCTTCTGCGAGCGAAGCCACCGACGC | 540 |
| Qy | 541 | CAGCGCGGACCAACACACCGGGCCCAACATCGGTGCGAGCCCTGTCCTGCGCC | 600 |
| Db | 541 | CAGCGCGGACCAACACACCGGGCCCAACATCGGTGCGAGCCCTGTCCTGCGCC | 600 |
| Qy | 601 | CAGGGCGTCCGGCCAGCGGGGGGCGCAGTGCACACGAGGGGGTGGACTTCGCGCT | 660 |
| Db | 601 | CAGGGCGTCCGGCCAGCGGGGGGCGCAGTGCACACGAGGGGGTGGACTTCGCGCT | 660 |
| Qy | 661 | GTGATATCTACTCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCACTGG | 720 |
| Db | 661 | GTGATATCTACTCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGTCACTGG | 720 |
| Qy | 721 | TTATCACCCTTTACTTGCACACACAGAACCGAAGACGTGTTTGCAAATGTCCCGGCTG | 780 |
| Db | 721 | TTATCACCCTTTACTTGCACACACAGAACCGAAGACGTGTTTGCAAATGTCCCGGCTG | 780 |
| Qy | 781 | TGGTCAAAATCGGGAGACAGCCAGCTTTTGGCGCAGATACGTCTAAACCTGTGCAACAG | 840 |
| Db | 781 | TGGTCAAAATCGGGAGACAGCCAGCTTTTGGCGCAGATACGTCTAAACCTGTGCAACAG | 840 |

| | | | |
|----|------|---|------|
| Qy | 841 | CCACTACATTAATCAAACTGAGATCCTTCTCTTTGAGGGAGCAAGTCCCTTCCCTTTCA | 900 |
| Db | 841 | CCACTACATTAATCAAACTGAGATCCTTCTCTTTGAGGGAGCAAGTCCCTTCCCTTTCA | 900 |
| Qy | 901 | TTTTTCCAGTCTTCCCTCGTGTATTCATCTCATGATTAATTTTAGTGGGGCGGG | 960 |
| Db | 901 | TTTTTCCAGTCTTCCCTCGTGTATTCATCTCATGATTAATTTTAGTGGGGCGGG | 960 |
| Qy | 961 | GTGGGAAAGATTAATCTTTTCTTTATGTGTGTGACGGGAAACAAACTAGGTAAATCTAC | 1020 |
| Db | 961 | GTGGGAAAGATTAATCTTTTCTTTATGTGTGTGACGGGAAACAAACTAGGTAAATCTAC | 1020 |
| Qy | 1021 | AGTACACACAAGGGTCAAAATACATGTTGTGCGGCAATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Db | 1021 | AGTACACACAAGGGTCAAAATACATGTTGTGCGGCAATCGCGGTAGGCGTGGAAAGGG | 1080 |
| Qy | 1081 | CAGCCAGAGCTACCCGAGAGTTCAGAAATCATGCTGAGAGAGCTGGAGCACCCATG | 1140 |
| Db | 1081 | CAGCCAGAGCTACCCGAGAGTTCAGAAATCATGCTGAGAGAGCTGGAGCACCCATG | 1140 |
| Qy | 1141 | CCATCTCAACCTCTTCCCGCCCGTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT | 1200 |
| Db | 1141 | CCATCTCAACCTCTTCCCGCCCGTTTACAAAGGGGAGGCTAAAGCCAGAGACAGCT | 1200 |
| Qy | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGACCTTGTCTCCA | 1260 |
| Db | 1201 | TGATCAAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGACCTTGTCTCCA | 1260 |
| Qy | 1261 | GCTCAGGGCTTCTTCCCAACCATTCAGGCTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Db | 1261 | GCTCAGGGCTTCTTCCCAACCATTCAGGCTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| Qy | 1321 | TGAGGTGCTTGAAGTCTCCAAAGGAAACAAAGTACTTCTTGATACCTGGGATACGT | 1380 |
| Db | 1321 | TGAGGTGCTTGAAGTCTCCAAAGGAAACAAAGTACTTCTTGATACCTGGGATACGT | 1380 |
| Qy | 1381 | GCCAGAGCTTCGAGGAGGTAAATGAAATTAAGAGAGAACTGCCCTTGGCAGAGTCTAT | 1440 |
| Db | 1381 | GCCAGAGCTTCGAGGAGGTAAATGAAATTAAGAGAGAACTGCCCTTGGCAGAGTCTAT | 1440 |
| Qy | 1441 | AATGTAACATATCAGACTTTTCTTATATATCAAGCCCTAAATGATAGACCTAA | 1500 |
| Db | 1441 | AATGTAACATATCAGACTTTTCTTATATCAAGCCCTAAATGATAGACCTAA | 1500 |
| Qy | 1501 | AATAAATGAAGTGGTGAAGCTTAAACCTGGAAAAATGATCCCTCTATCTCTAAAGAAAT | 1560 |
| Db | 1501 | AATAAATGAAGTGGTGAAGCTTAAACCTGGAAAAATGATCCCTCTATCTCTAAAGAAAT | 1560 |
| Qy | 1561 | CTCTGTGAACCCCTATGTGAGGGGAAATGCTCTCCAGCCCTTGATTCAGAGGGG | 1620 |
| Db | 1561 | CTCTGTGAACCCCTATGTGAGGGGAAATGCTCTCCAGCCCTTGATTCAGAGGGG | 1620 |
| Qy | 1621 | CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA | 1680 |
| Db | 1621 | CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA | 1680 |
| Qy | 1681 | CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAATGCTTCCTGGGATCAGTGATGA | 1740 |
| Db | 1681 | CTAAGGGCCCTCTTGAATCTCTGAATTTGAGATACAAATGCTTCCTGGGATCAGTGATGA | 1740 |
| Qy | 1741 | CTTTTATATCTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCAACAGCCCTGGCCCTGT | 1800 |
| Db | 1741 | CTTTTATATCTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCAACAGCCCTGGCCCTGT | 1800 |
| Qy | 1801 | CAATAGCAGATACAGGGATGAGCAGACCTGACTCTCTTAAGAGGGCTGAGAGCCCAA | 1860 |
| Db | 1801 | CAATAGCAGATACAGGGATGAGCAGACCTGACTCTCTTAAGAGGGCTGAGAGCCCAA | 1860 |
| Qy | 1861 | CTGCTGTCCCAAAACATGCACTTCTCTTCTTGAAGGTATGGTACAAAGCAATGCTGCCAAT | 1920 |
| Db | 1861 | CTGCTGTCCCAAAACATGCACTTCTCTTCTTGAAGGTATGGTACAAAGCAATGCTGCCAAT | 1920 |

QY 1921 GGAGAGAAAACTTAAGTAGATAGAGAAATAAGAACCACTCATATAATCTTCACTTAGG 1980
Db 1921 GGAGAGAAAACTTAAGTAGATAGAGAAATAAGAACCACTCATATAATCTTCACTTAGG 1980
QY 1981 AATAATCTCTGTTAATATGTTGATACATCTTCTGATTAATTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATACATCTTCTGATTAATTTCTACACATACATGTA 2040
QY 2041 AATATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2100
Db 2041 AATATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2100
QY 2101 AATATGTTGATGCTCTCTTTAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2160
Db 2101 AATATGTTGATGCTCTCTTTAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2160
QY 2161 AAAAAAATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2220
Db 2161 AAAAAAATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2220
QY 2221 AAAAAAATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2261
Db 2221 AAAAAAATGCTCTCTTTTAAATAGGTTGATGCTATGCTGTTATGAGTGGCTTTAATGAAT 2261

RESULT 2
AD592791
ID ADS92791 standard; cDNA; 2261 BP.
AC ADS92791;
DT 16-DEC-2004 (first entry)
DE Nucleotide sequence of a CD8 alpha-chain protein.
KW immune response; cell-specific antigen; alloantigen; CD8;
KW CD8 alpha-chain; cellular immune response; humoral immune response;
KW transplant allograft; graft-versus-host disease; transplanted; gene; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 120..827
FT /*tag= a
FT /product= "CD8 alpha-chain"
XX WO2004083244-A2.
XX 30-SEP-2004.
XX 19-MAR-2004; 2004WO-US008574.
XX 19-MAR-2003; 2003US-0456378P.
XX (ISOG-) ISOGENIS INC.
XX Qi Y, Zhang X, Konigsberg PJ;
XX WPI; 2004-691022/67.
XX P-PSDB; ADS92790.
XX Specifically inhibiting host immune responses to alloantigens, useful for
XX e.g. treating graft-versus-host disease, comprises contacting a target
XX cell expressing the antigen with an expression vector encoding a CD8
XX polypeptide.
XX Disclosure; Fig 1; 98pp; English.
XX The specification describes a method for specifically inhibiting a host
XX immune response to target cell-specific antigens (e.g. alloantigens). The
XX method comprises contacting a target cell expressing the antigen with an
XX expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX chain, where the CD8 polypeptide is expressed by the target cell and

[Handwritten signature]

CC where the host immune response against the target cell is specifically
CC inhibited. The method of the invention is useful for specifically
CC inhibiting both cellular and humoral immune responses to alloantigens,
CC thus finding use in extending the survival of transplant allografts, and
CC in treating graft-versus-host disease in transplant recipients. The
CC present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
CC -chain may be used in the method of the invention.
XX

SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;
Query Watch 100.0%; Score 2261; DB 13; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATCAGGCTCGGGCCGGGCGGAGGGGCGCAACTTTCCCTCGGCGCCACCGGCT 60
Db 1 GAAATCAGGCTCGGGCCGGGCGGAGGGGCGCAACTTTCCCTCGGCGCCACCGGCT 60
QY 61 CCGCGCGCTCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 120
Db 61 CCGCGCGCTCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA 120
QY 121 TGGCCTTACAGTACCGGCTTGTCTCCGCTGCGCTTGTCTGCTCCAGCGCCAGGC 180
Db 121 TGGCCTTACAGTACCGGCTTGTCTCCGCTGCGCTTGTCTGCTCCAGCGCCAGGC 180
QY 181 CGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAGC 240
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QY 241 TGAAGTGCAGGTGCTGCTGCTCCAAACCGACGCTCGGGCTGCTCGTGGCTTTCACGCCG 300
Db 241 TGAAGTGCAGGTGCTGCTGCTCCAAACCGACGCTCGGGCTGCTCGTGGCTTTCACGCCG 300
QY 301 GCGGCGCGCGCGCGAGTCCACTTCTCTATACCTTCTCCAAACCGACGCTCGGGCTGCTCGTGGCT 360
Db 301 GCGGCGCGCGCGCGAGTCCACTTCTCTATACCTTCTCCAAACCGACGCTCGGGCTGCTCGTGGCT 360
QY 361 CCGAGGGGCTGACACACCGGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTCA 420
Db 361 CCGAGGGGCTGACACACCGGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTCA 420
QY 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTTGAGCAACT 480
Db 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTTGAGCAACT 480
QY 481 CCATCATGTAATTCAGCCACTTCTGCGGCTTCTGCTGCGAGGAGCCACACGACGCG 540
Db 481 CCATCATGTAATTCAGCCACTTCTGCGGCTTCTGCTGCGAGGAGCCACACGACGCG 540
QY 541 CAGCGCGCGACCAACACACCGGCGCCACCATCGCTCGGAGCCCTGCTCCCTGCGCC 600
Db 541 CAGCGCGCGACCAACACACCGGCGCCACCATCGCTCGGAGCCCTGCTCCCTGCGCC 600
QY 601 CAGGCGCTGCGCGCGAGCGGCGGCGAGTGCACACGAGGGGGTGGAGCTTCGCT 660
Db 601 CAGGCGCTGCGCGCGAGCGGCGGCGAGTGCACACGAGGGGGTGGAGCTTCGCT 660
QY 661 GTGATATCTACATCTGGGCGGCTTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACTGG 720
Db 661 GTGATATCTACATCTGGGCGGCTTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACTGG 720
QY 721 TTATCACCCTTTACTGCAACACACGAGGAGCGTTTGGCAAAATGTCCTCCCGGCTG 780
Db 721 TTATCACCCTTTACTGCAACACACGAGGAGCGTTTGGCAAAATGTCCTCCCGGCTG 780
QY 781 TGGTCAAAATCGGAGACAAAGCCAGCTTTTGGCGAGATACGTCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAAGCCAGCTTTTGGCGAGATACGTCTAAACCTGTGCAACAG 840
QY 841 CCATCATGTAATTCAGCCACTTCTGCGGCTTCTGCTGCGAGGAGCCACAGTCTTCCTTCAT 900
Db 841 CCATCATGTAATTCAGCCACTTCTGCGGCTTCTGCTGCGAGGAGCCACAGTCTTCCTTCAT 900

CC immunogenicity. Accordingly, these compositions are useful for inhibiting
CC both the cellular and humoral components of the host immune responses
CC against expression vectors and target cells transfected with the vectors.
CC As such, they exhibit immunosuppressive activity. This polynucleotide is
CC the DNA sequence of the human CD8 alpha chain mRNA of the invention.
XX
SQ

Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 13; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | GAATCAGGCTCGGGCCGGCGAAGGGCGCAACTTTCCTCCCTCGGGCCCGCCACCGCT | 60 |
| DB | 1 | GAATCAGGCTCGGGCCGGCGAAGGGCGCAACTTTCCTCCCTCGGGCCCGCCACCGCT | 60 |
| QY | 61 | CCGCGCGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA | 120 |
| DB | 61 | CCGCGCGCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA | 120 |
| QY | 121 | TGGCCTTACAGTGACCGGCTTGCTCTCTCGCGCTGGCTTGCTCCACGCGCCGAGGC | 180 |
| DB | 121 | TGGCCTTACAGTGACCGGCTTGCTCTCTCGCGCTGGCTTGCTCCACGCGCCGAGGC | 180 |
| QY | 181 | CGAGCCAGTTCGGGTGTGCGCTGTGATCGGACTTGGAACTGGGGGAGACAGTGGAGC | 240 |
| DB | 181 | CGAGCCAGTTCGGGTGTGCGCGCTGATCGGACTTGGAACTGGGGGAGACAGTGGAGC | 240 |
| QY | 241 | TGAAGTGCCAGTGCTGCTCCACCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA | 300 |
| DB | 241 | TGAAGTGCCAGTGCTGCTCCACCCGAGCTTCGAGCCAAAGCAGCGTCTCGGGAGCGGTCA | 300 |
| QY | 301 | GGGGCCCGCCGACAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG | 360 |
| DB | 301 | GGGGCCCGCCGACAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG | 360 |
| QY | 361 | CGAGGGGTGACACCCAGCGGTTCTCGGCAAGAGTGGGGGACACCTTCGCTCTCA | 420 |
| DB | 361 | CGAGGGGTGACACCCAGCGGTTCTCGGCAAGAGTGGGGGACACCTTCGCTCTCA | 420 |
| QY | 421 | CCCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTCTCGGCCCTGAGCACT | 480 |
| DB | 421 | CCCTGAGCGACTTCGCGCGAGAGACGAGGGTACTATTCTCTCGGCCCTGAGCACT | 480 |
| QY | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGTTCTCTGCGAGAGCCACACGACGC | 540 |
| DB | 481 | CCATCATGTACTTCAGCCACTTCGTGCGGTTCTCTGCGAGAGCCACACGACGC | 540 |
| QY | 541 | CAGCGCGGACCAACACACCGGCGCCACCATCGCGTCGAGCCCTGTCCCTGGCGC | 600 |
| DB | 541 | CAGCGCGGACCAACACACCGGCGCCACCATCGCGTCGAGCCCTGTCCCTGGCGC | 600 |
| QY | 601 | CAGAGCGTGGCGGCGGCGGCGGCGAGTGCAACAGAGGGGCTGGACTTCGCT | 660 |
| DB | 601 | CAGAGCGTGGCGGCGGCGGCGGCGGCGAGTGCAACAGAGGGGCTGGACTTCGCT | 660 |
| QY | 661 | GTGATATCTACATCTGGGCGCTTCGCGGAGCTTGTGGGGTCTCTCTCTGCTACTGG | 720 |
| DB | 661 | GTGATATCTACATCTGGGCGCTTCGCGGAGCTTGTGGGGTCTCTCTCTGCTACTGG | 720 |
| QY | 721 | TTATCACTTTACTGCAACCAAGAGACCGTGTGTTGCAAAATGCTCCCGGCGCTG | 780 |
| DB | 721 | TTATCACTTTACTGCAACCAAGAGACCGTGTGTTGCAAAATGCTCCCGGCGCTG | 780 |
| QY | 781 | TGGTCAATTCGGAGACAGCCAGCTTTCGGCGAGTACGTCTAAACCTGTGCAACG | 840 |
| DB | 781 | TGGTCAATTCGGAGACAGCCAGCTTTCGGCGAGTACGTCTAAACCTGTGCAACG | 840 |
| QY | 841 | CCACTACATTTACTTCAAACTGAGATCTTCTTTTGGGGGACAGTCTTCCCTTTCAT | 900 |
| DB | 841 | CCACTACATTTACTTCAAACTGAGATCTTCTTTTGGGGGACAGTCTTCCCTTTCAT | 900 |
| QY | 901 | TTTTTCCAGTCTTCTCCTGTGTATTCATCTCATGATTAATTTTAGTGGGGCGGG | 960 |

| | | | |
|----|------|--|------|
| DB | 901 | TTTTTCCAGTCTTCTCCTGTGTATTCATCTCATGATTAATTTTAGTGGGGCGGG | 960 |
| QY | 961 | GTGGGAAAGATTACTTTTTTATATGTGTTCACGGGAAACAAAACCTAGGTAATCTAC | 1020 |
| DB | 961 | GTGGGAAAGATTACTTTTTTATATGTGTTCACGGGAAACAAAACCTAGGTAATCTAC | 1020 |
| QY | 1021 | AGTACACCACAAGGGTCACAATACCTTGTGTGGGCACATCGCGTAGGGCTGGAAGGGG | 1080 |
| DB | 1021 | AGTACACCACAAGGGTCACAATACCTTGTGTGGGCACATCGCGTAGGGCTGGAAGGGG | 1080 |
| QY | 1081 | CAGGCCAGAGCTACCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATG | 1140 |
| DB | 1081 | CAGGCCAGAGCTACCGCAGAGTTCTCAGAATCATGCTGAGAGAGCTGGAGGCACCCATG | 1140 |
| QY | 1141 | CCATCTCAACCTCTTCCCGCCGCTTTTACAAGGGGAGGCTTAAAGCCAGAGACAGCT | 1200 |
| DB | 1141 | CCATCTCAACCTCTTCCCGCCGCTTTTACAAGGGGAGGCTTAAAGCCAGAGACAGCT | 1200 |
| QY | 1201 | TGATCAAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| DB | 1201 | TGATCAAAAGGCACACAGCAAGTCAGGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| QY | 1261 | GCTCAGGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| DB | 1261 | GCTCAGGGCTCTTCTCTCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG | 1320 |
| QY | 1321 | TGAGGTGCTTGTAGTCTCCAAACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT | 1380 |
| DB | 1321 | TGAGGTGCTTGTAGTCTCCAAACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT | 1380 |
| QY | 1381 | GCCGAGAGCTCGAGGAGTAAATGAAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT | 1440 |
| DB | 1381 | GCCGAGAGCTCGAGGAGTAAATGAAATTAAGAGAGAACTGCTTTGGCAGAGTTCTAT | 1440 |
| QY | 1441 | AATGTAACAATATCAGACTTTTTTTTTTATAAACAAGCCCTAAATTTGATAGACCTAA | 1500 |
| DB | 1441 | AATGTAACAATATCAGACTTTTTTTTTTATAAACAAGCCCTAAATTTGATAGACCTAA | 1500 |
| QY | 1501 | AATAAATGAGTGTGAGCTTAAACCTCGGAAATGAAATCCCTCTATCTCTAAGGAAAT | 1560 |
| DB | 1501 | AATAAATGAGTGTGAGCTTAAACCTCGGAAATGAAATCCCTCTATCTCTAAGGAAAT | 1560 |
| QY | 1561 | CTCTGTGAAACCCCTATGTGGAGGCGGAAATGCTCTCCAGGCCCTTGATTCAGAGGGG | 1620 |
| DB | 1561 | CTCTGTGAAACCCCTATGTGGAGGCGGAAATGCTCTCCAGGCCCTTGATTCAGAGGGG | 1620 |
| QY | 1621 | CCCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAA | 1680 |
| DB | 1621 | CCCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAA | 1680 |
| QY | 1681 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCAGTATGA | 1740 |
| DB | 1681 | CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCAGTATGA | 1740 |
| QY | 1741 | CTTTTATATCTTTGTAAGACAAATTTGGAGAGCCCTCACACAGCCCTGCGCTCTGCT | 1800 |
| DB | 1741 | CTTTTATATCTTTGTAAGACAAATTTGGAGAGCCCTCACACAGCCCTGCGCTCTGCT | 1800 |
| QY | 1801 | CAACTAGCAGATACAGGATGAGGACCTGACTCTCTTAAAGAGGCTGAGAGCCCAAA | 1860 |
| DB | 1801 | CAACTAGCAGATACAGGATGAGGACCTGACTCTCTTAAAGAGGCTGAGAGCCCAAA | 1860 |
| QY | 1861 | CTGCTGTCCCAACATGCACTTCTTGAAGTATGGTACCAAGCAATGCTTCCCTT | 1920 |
| DB | 1861 | CTGCTGTCCCAACATGCACTTCTTGAAGTATGGTACCAAGCAATGCTTCCCTT | 1920 |
| QY | 1921 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAAGAACCACTCATTAATCTTCCACCTTAGG | 1980 |
| DB | 1921 | GGAGAGAAAAAATTAAGTAGATAAGGAAATAAGAACCACTCATTAATCTTCCACCTTAGG | 1980 |
| QY | 1981 | AATAATCTCTGTATATGTTGATCAATTTCTCTGATTAATTTCTACACATACATGTA | 2040 |

Db 1981 AATAATCTCTGTTAATAATGTTGATACATTTCTCTGATATTATTTTCTACATACATGTAA 2040
Qy
2041 AATATGCTCTTTCTTTTAAATAGGTTGTAATACTATGCTGTTATGAGTGCGCTTTAATGAAT 2100
Db 2041 AATATGCTCTTTCTTTTAAATAGGTTGTAATACTATGCTGTTATGAGTGCGCTTTAATGAAT 2100
Qy 2101 AAACATTTGTAGCATCTCTTTAATGTTGTAATACTATGCTGTTATGAGTGCGCTTTAATGAAT 2160
Db 2101 AAACATTTGTAGCATCTCTTTAATGTTGTAATACTATGCTGTTATGAGTGCGCTTTAATGAAT 2160
Qy 2161 AA 2220
Db 2161 AA 2220
Qy 2221 AA 2261
Db 2221 AA 2261

RESULT 4
ADW86779
ID ADW86779 standard; DNA; 2261 BP.
XX AC ADW86779;
XX DT 07-APR-2005 (first entry)
XX DE Human CD8 gene.
XX KW protein interaction; fusion protein; ss; PCR; primer.
XX OS Homo sapiens.
XX PN WO2005007822-A2.
XX PD 27-JAN-2005.
XX PF 09-JUL-2004; 2004WO-US021887.
XX PR 09-JUL-2003; 2003US-0485968P.
XX PR 15-OCT-2003; 2003US-0511918P.
XX PR 27-APR-2004; 2004US-0566113P.
XX (SENT-) SENTIGEN BIOSCIENCES INC.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Lee KJ, Axel R, Strapps W, Barnea G;
XX WPT; 2005-102091/11.
XX DR

Determining protein/protein interaction modulator comprises contacting the compound to a cell transformed or transfected with G-protein coupled receptor and arrestin.
Example 29; SEQ ID NO 99; 133pp; English.
The invention relates to a novel method for determining if a test-compound modulates a specific protein/protein interaction or protein interactions of interest. The method comprises contacting the compound to a cell or samples of cells, each of which has been transformed or transfected with a nucleic acid molecule. The invention further comprises: a recombinant cell, transformed or transfected with any of the nucleic acid molecules; an isolated nucleic acid molecule comprising, in 5' to 3' order, any of the nucleotide sequences described; an expression vector comprising the isolated nucleic acid molecule of above, operably linked to a promoter; a fusion protein produced by expression of the isolated nucleic acid molecule of above; and a test kit, useful for determining if a test compound modulates a specific protein/protein interaction of interest. The methods, nucleic acid molecules, and kit are useful for determining if a test-compound modulates a specific protein/protein interaction or protein interactions of interest. This polynucleotide sequence represents the human CD8 gene used in the method of the invention.

W-1/2006

XX SQ Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;
Query Match 100.0%; Score 2261; DB 14; Length 2261;
Best Local Similarity 100.0%; Pred. No. 1.8e-308;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAATCAGGCTCCGGGCGCGGCGGAGGCGCAACTTTTCCCTCGGGCGCCACCGGCT 60
Db 1 GAATCAGGCTCCGGGCGCGGCGGAGGCGCAACTTTTCCCTCGGGCGCCACCGGCT 60
Qy 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCAGGCAAGCAGCGCTCTGGGAGCGCGTCA 120
Db 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCAGGCAAGCAGCGCTCTGGGAGCGCGTCA 120
Qy 121 TGGCCTTACCACTGACCGCTTGTCTCTGCGCGCTTGTCTGCTCACCGCGCAGGC 180
Db 121 TGGCCTTACCACTGACCGCTTGTCTCTGCGCGCTTGTCTGCTCACCGCGCAGGC 180
Qy 181 CGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGAACTTGGAACTTGGGCGGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGAACTTGGAACTTGGGCGGAGACAGTGGAGC 240
Qy 241 TGAAGTGCAGGCTGCTGCTGTCACACCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
Db 241 TGAAGTGCAGGCTGCTGCTGTCACACCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
Qy 301 GCGGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG 360
Db 301 GCGGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAACAGCCCAAGGCGG 360
Qy 361 CGAGGGGCTGGACACCCAGCGGTTCTGGGCAAGAGTTGGGGGACACCTTCGTCCTCA 420
Db 361 CGAGGGGCTGGACACCCAGCGGTTCTGGGCAAGAGTTGGGGGACACCTTCGTCCTCA 420
Qy 421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGGCTCGAGCAACT 480
Db 421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGCTACTATTCTGCTCGGCTCGAGCAACT 480
Qy 481 CCATCATGTACTTCAGCCACTTCGTCGCGGCTTCTCTGCCAGGAGCCCAACAGCGC 540
Db 481 CCATCATGTACTTCAGCCACTTCGTCGCGGCTTCTCTGCCAGGAGCCCAACAGCGC 540
Qy 541 CAGCGCGCGGAGCAACACCGGCGCCACATGCGCTCGAGCCCTGTCCTCGCGCC 600
Db 541 CAGCGCGCGGAGCAACACCGGCGCCACATGCGCTCGAGCCCTGTCCTCGCGCC 600
Qy 601 CAGAGGCGTGGCGCGCGGCGCGGCGGAGTGCACACGAGGGGGCTGGACTTCGCT 660
Db 601 CAGAGGCGTGGCGCGCGGCGCGGCGGAGTGCACACGAGGGGGCTGGACTTCGCT 660
Qy 661 GTGATATCTACATCTGGGCGCGCTTGGCGGCGCTTGTGGGGTCTTCTCTGTCACTGG 720
Db 661 GTGATATCTACATCTGGGCGCGCTTGGCGGCGCTTGTGGGGTCTTCTCTGTCACTGG 720
Qy 721 TTATCACTCTTACTGCAACCAAGAGCTTTTGGCAAAAGTCCCGGCGCTG 780
Db 721 TTATCACTCTTACTGCAACCAAGAGCTTTTGGCAAAAGTCCCGGCGCTG 780
Qy 781 TGGTCAAAATCGGAGACAAGCCAGCCCTTCGCGGAGATACGTCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAGCCAGCCCTTCGCGGAGATACGTCTAAACCTGTGCAACAG 840
Qy 841 CCATCATATTTCTTCAAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCCCTTCAT 900
Db 841 CCATCATATTTCTTCAAACTGAGATCTTCTCTTTGAGGGAGCAAGTCTTCCCTTCAT 900
Qy 901 TTTTTCAGTCTTCTCTCTGATTTCAATCTCATGATTTATTTTAGTGGGCGGG 960
Db 901 TTTTTCAGTCTTCTCTCTGATTTCAATCTCATGATTTATTTTAGTGGGCGGG 960
Qy 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGGCGGAAACAAAACACTAGGTAAATCTTAC 1020
Db 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGGCGGAAACAAAACACTAGGTAAATCTTAC 1020

Db 961 GTGGGAAGATTAATCTTTTCTTTATGTGTGTTGACGGGAACAAAACTAGGTAAAAATCTAC 1020
QY 1021 AGTACACCAAGGGTCAACAATACTGTGTGCGCACATCGCGGTAGGGGTGAAAGGGG 1080
Db 1021 AGTACACCAAGGGTCAACAATACTGTGTGCGCACATCGCGGTAGGGGTGAAAGGGG 1080
QY 1081 CAGGCCAGAGCTACCCGCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGAGGGCACCCATG 1140
Db 1081 CAGGCCAGAGCTACCCGCGAGAGTCTCAGAAATCATGCTGAGAGAGCTGAGGGCACCCATG 1140
QY 1141 CCAATCTCAACCTCTTCCCGCGCGTCTTACAAAGGGGGAGGCTAAAGCCAGAGACAGCT 1200
Db 1141 CCAATCTCAACCTCTTCCCGCGCGTCTTACAAAGGGGGAGGCTAAAGCCAGAGACAGCT 1200
QY 1201 TGATCAAGGCAACACAGCAAGTCAAGGTTGGAGCAGTAGCTGAGGGAACCTGTCTCCCA 1260
Db 1201 TGATCAAGGCAACACAGCAAGTCAAGGTTGGAGCAGTAGCTGAGGGAACCTGTCTCCCA 1260
QY 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTCTTTCTTCCGAGGCCCTGTCTCAGGG 1320
Db 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTCTTTCTTCCGAGGCCCTGTCTCAGGG 1320
QY 1321 TGAGGTGCTTGAGTCTCCAAAGGCAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT 1380
Db 1321 TGAGGTGCTTGAGTCTCCAAAGGCAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT 1380
QY 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Db 1381 GCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCTAAATTTGATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCTAAATTTGATAGACCTAA 1500
QY 1501 AATATAAGTGGTGGCTTAACCTCGAAATGAATCCCTCTATCTCTTAAGAAAT 1560
Db 1501 AATATAAGTGGTGGCTTAACCTCGAAATGAATCCCTCTATCTCTTAAGAAAT 1560
QY 1561 CTCCTGAAACCCCTATGTGGAGGGCGAATGTCTCTCCAGGCCCTTGCAATGAGAGGG 1620
Db 1561 CTCCTGAAACCCCTATGTGGAGGGCGAATGTCTCTCCAGGCCCTTGCAATGAGAGGG 1620
QY 1621 CCCATGAAGAGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCAATCAGTAGGTTAA 1680
Db 1621 CCCATGAAGAGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCAATCAGTAGGTTAA 1680
QY 1681 CTAAGGCCCTCTGATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATCA 1740
Db 1681 CTAAGGCCCTCTGATCTCTGAATTTGAGATACAAACATGTTCTGGGATCACTGATCA 1740
QY 1741 CTTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT 1800
Db 1741 CTTTTTATATCTTTGTAAGACAAATTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT 1800
QY 1801 CAACTAGCAGATACAGGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
Db 1801 CAACTAGCAGATACAGGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
QY 1861 CTGCTGTCCCAACATGCACTCTCTGCTTAAGGTATGTTAGCAAGCAATGCCTGCCATT 1920
Db 1861 CTGCTGTCCCAACATGCACTCTCTGCTTAAGGTATGTTAGCAAGCAATGCCTGCCATT 1920
QY 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATATCTTCCACCTTAGG 1980
Db 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATATCTTCCACCTTAGG 1980
QY 1981 AATAATCTCTGTTAATATGTTGATCTTCTCTGATTAATTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATCTTCTCTGATTAATTTCTACACATACATGTA 2040
QY 2041 AATATGCTCTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAAT 2100
Db 2041 AATATGCTCTCTTTTAAATAGGGTTGATCTATGCTGTTATGAGTGGCTTTAATGAAT 2100

QY 2101 AAACATTTTAGCATCTCTTTAATGGTAAACAGCAAAAAA 2160
Db 2101 AAACATTTTAGCATCTCTTTAATGGTAAACAGCAAAAAA 2160
QY 2161 AAAAAA 2220
Db 2161 AAAAAA 2220
QY 2221 AAAAAA 2261
Db 2221 AAAAAA 2261

RESULT 5

ID AD226401

XX AD226401 standard; cDNA; 2261 BP.

AC AD226401;

XX 16-JUN-2005 (first entry)

DX Human CD8 cDNA.

DE cell culture; stem cell; CD8; ss; gene.

XX Homo sapiens.

XX WO2005030999-A1.

XX 07-APR-2005.

XX 24-SEP-2004; 2004WO-US031524.

PR 25-SEP-2003; 2003US-0506221P.

PR 08-OCT-2003; 2003US-0509594P.

XX (DAND) DANA FARBER CANCER INST INC.

XX Ritz J, Wu CJ;

DR WPI; 2005-273394/28.

DR P-PSDB; AD226402.

XX Detecting lineage-specific cells in a biological sample, useful for determining the clinical outcome of a progenitor cell transfer in a subject, comprises identifying lineage-specific mRNA in the sample.

PS Disclosure; SBQ ID NO 27; 393pp; English.

XX The invention relates to a method of detecting lineage-specific cells in a biological sample which comprises identifying lineage-specific mRNA in the sample. The methods are useful for determining the clinical outcome of a progenitor cell transfer in a subject, and for identifying or quantifying lineage-specific cells. The present sequence represents a human cDNA that encodes a protein used to identify lineage-specific cells.

XX Sequence 2261 BP; 626 A; 599 C; 531 G; 505 T; 0 U; 0 Other;

Query Match 100.0%; Score 2261; DB 14; Length 2261;

Best Local Similarity 100.0%; Pred. No. 1.8e-308;

Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATCAGGCTCCGGGCGGCGAAGGGCGCAACTTTCCCTCGGCGCCCAACCGGCT 60

Db 1 GAAATCAGGCTCCGGGCGGCGAAGGGCGCAACTTTCCCTCGGCGCCCAACCGGCT 60

QY 61 CCCGCGCCCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCGCTCTGGGAGCGGTCA 120

Db 61 CCCGCGCCCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCGCTCTCTGGGAGCGGTCA 120

QY 121 TGGCCTTACCACTGACCGGCTTGTCTCCCTCGGCTTGTCTCCACGCGCGCAGGC 180

N6 - Jute

Db 121 TGGCCTTACCAAGTGAACCGCCTTGCTCCGCGCTGGCCCTTGCTGCTCACGCCGCCAGGC 180
Qy 181 CGAGCCAGTTCGGGTGTGCGCGCTGGATCGGAACCTGGAACTCGGGCGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCGGGTGTGCGCGCTGGATCGGAACCTGGAACTCGGGCGAGACAGTGGAGC 240
Qy 241 TGAAGTGCAGGTGTGCTGTCCAAACCGAGCGTGGGGCTGCTGTGGCTCTTCCAGCGCGC 300
Db 241 TGAAGTGCAGGTGTGCTGTCCAAACCGAGCGTGGGGCTGCTGTGGCTCTTCCAGCGCGC 300
Qy 301 GCGGCGCGCGCGAGTCCCACTTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
Db 301 GCGGCGCGCGCGAGTCCCACTTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
Qy 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTGGGGGACACCTTCGCTCTCA 420
Db 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTGGGGGACACCTTCGCTCTCA 420
Qy 421 CCCTGAGCGAATTTCGGCGAGAGAACGAGGGCTACTATTTCTGTGCGGCCCTGAGCAACT 480
Db 421 CCCTGAGCGAATTTCGGCGAGAGAACGAGGGCTACTATTTCTGTGCGGCCCTGAGCAACT 480
Qy 481 CCATCATGTACTTCAGCCACTTCGTGCGCGGTTCTCCGCAAGAGGTGGGGGACACCTTCGCTCTCA 540
Db 481 CCATCATGTACTTCAGCCACTTCGTGCGCGGTTCTCCGCAAGAGGTGGGGGACACCTTCGCTCTCA 540
Qy 541 CAGGCGCGGACACCAACCGCGCGCCACCATCGCGTCGAGCGCCCTGCTCCCTGCGCC 600
Db 541 CAGGCGCGGACACCAACCGCGCGCCACCATCGCGTCGAGCGCCCTGCTCCCTGCGCC 600
Qy 601 CAGAGGCGTGGCGGACGCGCGGGGGCGCAAGTGCAACAGAGGGGGCTGGACTTCGCGCT 660
Db 601 CAGAGGCGTGGCGGACGCGCGGGGGCGCAAGTGCAACAGAGGGGGCTGGACTTCGCGCT 660
Qy 661 GTGATATCTACATCTGGCGGCTTGGCGGGGACTTGGGGGTCTCTCTGCTGCACTGG 720
Db 661 GTGATATCTACATCTGGCGGCTTGGCGGGGACTTGGGGGTCTCTCTGCTGCACTGG 720
Qy 721 TTATCACCCCTTTACTGCAACCAACAGAAACCGAAGACGTGTTTGCAAATGTCCCGGCGCTG 780
Db 721 TTATCACCCCTTTACTGCAACCAACAGAAACCGAAGACGTGTTTGCAAATGTCCCGGCGCTG 780
Qy 781 TGGTCAAAATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAGCCAGCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAG 840
Qy 841 CCACCTACATTTACTCAAACTGAGATCCTTCTTTTGGGAGCAAGTCTTCCCTTTTCA 900
Db 841 CCACCTACATTTACTCAAACTGAGATCCTTCTTTTGGGAGCAAGTCTTCCCTTTTCA 900
Qy 901 TTTTTCAGTCTTCTCCCTGTGATTCATTTCTCATGATTAATTTAGTGGGGCGGG 960
Db 901 TTTTTCAGTCTTCTCCCTGTGATTCATTTCTCATGATTAATTTAGTGGGGCGGG 960
Qy 961 GTGGAAAGAATTACTTTTCTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTAC 1020
Db 961 GTGGAAAGAATTACTTTTCTTTATGTGTTGACGGGAAACAAAACCTAGGTAAATCTAC 1020
Qy 1021 AGTACACCAAGGGTCAATACCTGTTGCGCACATCGCGGTAGGCGGTGGAAGGGG 1080
Db 1021 AGTACACCAAGGGTCAATACCTGTTGCGCACATCGCGGTAGGCGGTGGAAGGGG 1080
Qy 1081 CAGGCGAGAGTACCCGCGAGAGTCTCAGAACTCATGCTGAGAGAGCTGGAGGCAACCCATG 1140
Db 1081 CAGGCGAGAGTACCCGCGAGAGTCTCAGAACTCATGCTGAGAGAGCTGGAGGCAACCCATG 1140
Qy 1141 CCATCTCAACTCTTTCGCGCGCGGTTTACAAAGGGGAGGCTAAAGCCGAGAGCAGCT 1200
Db 1141 CCATCTCAACTCTTTCGCGCGCGGTTTACAAAGGGGAGGCTAAAGCCGAGAGCAGCT 1200
Qy 1201 TGATCAAAAGGCACACAGCAAGTTCAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1260

Db 1201 TGATCAAAAGGCACACAGCAAGTTCAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1260
Qy 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCTTGTCTCAGGG 1320
Db 1261 GCTCAGGGCTCTTTCTCCACACCATTCAGGTCTTTCTTTCCGAGGCCCTTGTCTCAGGG 1320
Qy 1321 TGAGGTCTTGAGTCTCCNACGGCAAGGACAGTACTTCTTGATACCTCGGATACGT 1380
Db 1321 TGAGGTCTTGAGTCTCCNACGGCAAGGAAACAGTACTTCTTGATACCTCGGATACGT 1380
Qy 1381 GCCCAGAGCCTCGAGGAGTAAATGAATTAAGAAAGAGAACTGGCCTTTGGCAGAGTCTAT 1440
Db 1381 GCCCAGAGCCTCGAGGAGTAAATGAATTAAGAAAGAGAACTGGCCTTTGGCAGAGTCTAT 1440
Qy 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGTATAGACTTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCTTAAATTTGTATAGACTTAA 1500
Qy 1501 AATAAATGAAGTGGTGAAGTAAACCTGGAAATGAATCCCTCTATCTTAAAGAAAT 1560
Db 1501 AATAAATGAAGTGGTGAAGTAAACCTGGAAATGAATCCCTCTATCTTAAAGAAAT 1560
Qy 1561 CTCTGTGAAACCCCTATGTGGAGGGGAAATTTGCTCTCCAGGCCCTTGCATTTGCAGAGGG 1620
Db 1561 CTCTGTGAAACCCCTATGTGGAGGGGAAATTTGCTCTCCAGGCCCTTGCATTTGCAGAGGG 1620
Qy 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Qy 1681 CTAAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTTGGGATCAGTGATGA 1740
Db 1681 CTAAAGGCCCTCTTGAATCTCTGAATTTGAGATCAAAACATGTTCTTGGGATCAGTGATGA 1740
Qy 1741 CTTTATTACTTTGTAAAGACAAATTTTGGAGAGCCCTCACACAGCCCTGGCCTCTGCT 1800
Db 1741 CTTTATTACTTTGTAAAGACAAATTTTGGAGAGCCCTCACACAGCCCTGGCCTCTGCT 1800
Qy 1801 CAACTAGCAGATACAGGATGAGGACACCTGCACTCTCTTAAAGAGGCTGAGAGCCCAAA 1860
Db 1801 CAACTAGCAGATACAGGATGAGGACACCTGCACTCTCTTAAAGAGGCTGAGAGCCCAAA 1860
Qy 1861 CTGCTGTCCCAACATGCACCTCTTCTTAAAGGTATGATCAAGCAATGCTTCCCATTT 1920
Db 1861 CTGCTGTCCCAACATGCACCTCTTCTTAAAGGTATGATCAAGCAATGCTTCCCATTT 1920
Qy 1921 GGAGAGAAAACTTAAAGTAGATAAGGAAATAAGAACCACTCATAATTTCTTCCCTTAGG 1980
Db 1921 GGAGAGAAAACTTAAAGTAGATAAGGAAATAAGAACCACTCATAATTTCTTCCCTTAGG 1980
Qy 1981 AATAATCTCTGTTAAATAGGTGATACATTTCTTCTGATTAATTTCTACACATATGTA 2040
Db 1981 AATAATCTCTGTTAAATAGGTGATACATTTCTTCTGATTAATTTCTACACATATGTA 2040
Qy 2041 AATATGCTTTCTTTTAAATAGGTTGATGATGCTTATGCTTATGATGCTTTTAAATGA 2100
Db 2041 AATATGCTTTCTTTTAAATAGGTTGATGATGCTTATGCTTATGATGCTTTTAAATGA 2100
Qy 2101 AAAATTTGTAGCATCTCTTTTAAATAGGTTAAACAGCAAAAAAAGGAAAAAAGGAAAA 2160
Db 2101 AAAATTTGTAGCATCTCTTTTAAATAGGTTAAACAGCAAAAAAAGGAAAAAAGGAAAA 2160
Qy 2161 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2220
Db 2161 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2220
Qy 2221 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2261
Db 2221 AAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG 2261

| | | | | | |
|----|---|----|------|---|------|
| ID | ADQ64633 standard; cDNA; 3048 BP. | QY | 301 | GCGCGCGCGCGCGAGTCCACCTCTCCCTATATCTCTCCCAAAACAGCCCAAGCGCG | 360 |
| XX | AC | DB | 1213 | GGGGCGCGCGCGAGTCCACCTCTCTCTATATCTCTCCCAAAACAGCCCAAGCGCG | 1272 |
| XX | ADQ64633; | | | | |
| DT | 07-OCT-2004 (first entry) | QY | 361 | CGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCGTCTCTCA | 420 |
| XX | Novel human cDNA sequence #1794. | DB | 1273 | CCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCGTCTCTCA | 1332 |
| XX | | | | | |
| KW | ss; gene; osteoprotective; neuroprotective; nootropic; antiparkinsonian; | QY | 421 | CCCTGAGCGACTTCCGCGGAGAGAAACGAGGGCTACTATTCTCTCGGCGCTGAGCAACT | 480 |
| KW | cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; | DB | 1333 | CCCTGAGCGACTTCCGCGGAGAGAAACGAGGGCTAGTATTCTCTCGGCGCTGAGCAACT | 1392 |
| KW | neurological disease; Alzheimer's disease; Parkinson's disease; dementia; | | | | |
| KW | cancer. | | | | |
| XX | | | | | |
| OS | Homo sapiens. | QY | 481 | CCATCATGTATCTTCAGCCACTTTCGTGCGGTTCTTCTGCCAGCAAGCCACACAGACGC | 540 |
| XX | | DB | 1393 | CCATCATGTATCTTCAGCCACTTTCGTGCGGTTCTTCTGCCAGCAAGCCACACAGACGC | 1452 |
| PN | EP1440981-A2. | | | | |
| XX | | QY | 541 | CAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGCGAGCCCTTCCTTCGCGC | 600 |
| PD | 28-JUL-2004. | DB | 1453 | CAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGCGAGCCCTTCCTTCGCGC | 1512 |
| XX | | | | | |
| PF | 21-JAN-2004; 2004EP-00001196. | QY | 601 | CAGGCGCTGCG | 660 |
| XX | | DB | 1513 | CAGGCGCTGCG | 1572 |
| PR | 21-JAN-2003; 2003JP-00102205. | | | | |
| PR | 09-MAY-2003; 2003JP-00131392. | QY | 661 | GTGATATCTACATCTGGCGCGCTTGGCGCGGACTTTGTGGGTCCTTCTCTGTCACTGG | 720 |
| XX | (REAS-) RES ASSOC BIOTECHNOLOGY. | DB | 1573 | GTGATATCTACATCTGGCGCGCTTGGCGCGGACTTTGTGGGTCCTTCTCTGTCACTGG | 1632 |
| XX | | | | | |
| PI | Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S; | QY | 721 | TTATCACCCCTTTACTGCAACACACAGGAAACCGAGCGTTTGGCAAAATGTCCCGCGCTG | 780 |
| PI | Yamamoto J, Isono Y, Nagai K, Irie R; | DB | 1633 | TTATCACCCCTTTACTGCAACACACAGGAAACCGAGCGTTTGGCAAAATGTCCCGCGCTG | 1692 |
| XX | | | | | |
| DR | WPI; 2004-535376/52. | QY | 781 | TGCTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG | 840 |
| XX | P-PSDB; ADQ66821. | DB | 1693 | TGCTCAAAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGCTTAAACCTGTGCAACAG | 1752 |
| XX | | | | | |
| PT | Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, | QY | 841 | CCACTACATTAATCTCAAACTGAGATCTTCTCTCTTTGAGGAGCAAGTCTTCCCTTTCTAT | 900 |
| PT | Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. | DB | 1753 | CCACTACATTAATCTCAAACTGAGATCTTCTCTCTTTGAGGAGCAAGTCTTCCCTTTCTAT | 1812 |
| XX | Claim 1; SEQ ID NO 1794; 2449pp; English. | | | | |
| CC | The invention relates to 2495 novel polynucleotides (I) and their encoded | QY | 901 | TTTTTCCAGTCTTCTCTCTCTGTATTCATCTCATGATTAATATTATTAGTGGGCGGG | 960 |
| CC | polypeptides, sequences hybridizing to these nucleotides, sequences | DB | 1813 | TTTTTCCAGTCTTCTCTCTCTGTATTCATCTCATGATTAATATTATTAGTGGGCGGG | 1872 |
| CC | encoding partial polypeptides and sequences having 70% or 90% identity to | | | | |
| CC | the nucleotide and protein sequences. The nucleotides and polypeptides | QY | 961 | GTGGGAAAGATTACTTTTTTCTTTATGTGTGTGACGGGAAACAAAATCTAGTAAATCTAC | 1020 |
| CC | are useful as diagnostic markers or therapeutic target for the diseases | DB | 1873 | GTGGGAAAGATTACTTTTTTCTTTTATGTGTGTGACGGGAAACAAAATCTAGTAAATCTAC | 1932 |
| CC | or morbid states. They are also useful for treating osteoporosis, | | | | |
| CC | neurological diseases, Alzheimer's diseases, Parkinson's diseases, | QY | 1021 | AGTACACCAAGGGTCACAATATCTGTTGTGCGCATCTCGCGGTAGGGCGTGGAAAGGGG | 1080 |
| CC | dementia and various cancers. This sequence corresponds to a nucleotide | DB | 1933 | AGTACACCAAGGGTCACAATATCTGTTGTGCGCATCTCGCGGTAGGGCGTGGAAAGGGG | 1992 |
| CC | sequence of the invention. | | | | |
| XX | | QY | 1081 | CAGGCGAGCTACCCGCGAGATTCTCAGATCATCTGAGAGAGCTGGAGGACCCCATG | 1140 |
| SQ | Sequence 3048 BP; 659 A; 926 C; 771 G; 692 T; 0 U; 0 Other; | DB | 1993 | CAGGCGAGCTACCCGCGAGATTCTCAGATCATCTGAGAGAGCTGGAGGACCCCATG | 2052 |
| | | QY | 1141 | CCATCTCAACTCTTCTCCCGCGCGTTTTCACAAAGGGGAGGCTAAAGCCACAGACAGCT | 1200 |
| | | DB | 2053 | CGGTCTCAACTCTTCTCCCGCGCGTTTTCACAAAGGGGAGGCTAAAGCCACAGACAGCT | 2112 |
| | | QY | 1201 | TGATCAAAAGGCACACAGCAAGTTCAGGTTGGAGCATGAGCTGGAGGACCTTGTCTCCA | 1260 |
| | | DB | 2113 | TGATCAAAAGGCACACAGCAAGTTCAGGTTGGAGCATGAGCTGGAGGACCTTGTCTCCA | 2172 |
| | | QY | 1261 | GCTCAGGCTCTTCTCTCACACATTTCAGGTCTTTTCTTTTCGAGGCGCTGTCTCAGGG | 1320 |
| | | DB | 2173 | GCTCAGGCTCTTCTCTCACACATTTCAGGTCTTTTCTTTTCGAGGCGCTGTCTCAGGG | 2232 |
| | | QY | 1321 | TGAGTGTCTCAGTCTCCACGCGAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT | 1380 |
| | | DB | 2233 | TGAGTGTCTCAGTCTCCACGCGAAGGGAACAAGTACTTCTTGATACCTGGGATCTGT | 2292 |
| | | QY | 1381 | GCCAGAGCCTCGAGGAGTAAATGAATTAAGAAAGAGAACTGCCTTTTGGCAGAGTTCTAT | 1440 |

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Db 2293 G C C C A G A G C C T C G A G A G G T A A T G A A T T A A A G A G A G A C T G C C T T T T G C C A G A G T T C T A T 2352
Qy 1441 A A T G T A A C A A T A T C A G A C T T T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 1500
Db 2353 A A T G T A A C A A T A T C A G A C T T T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 2412
Qy 1501 A A T A A A T G A A G T G T A G C T T A C C C T G G A A A A T G A A T C C C T A T A T C T C T A A A G A A A T 1560
Db 2413 A A T A A A T G A A G T G T A G C T T A C C C T G G A A A A T G A A T C C C T A T A T C T C T A A A G A A A T 2472
Qy 1561 C T C T G T G A A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1620
Db 2473 C T C T G T G A A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 2532
Qy 1621 C C C A T G A A G A G G A C A G C T A C C C C T T A C A A A T A G A A T T T G A G C A T C A G T G A G T T A A A 1680
Db 2533 C C C A T G A A G A G G A C A G C T A C C C C T T A C A A A T A G A A T T T G A G C A T C A G T G A G T T A A A 2592
Qy 1681 C T A A G G C C C T T T G A A T C T T G A A T T T G A G A T A C A A A C A T G T T C T G G A T C A C T G A T G A 1740
Db 2593 C T A A G G C C C T T T G A A T C T T G A A T T T G A G A T A C A A A C A T G T T C T G G A T C A C T G A T G A 2652
Qy 1741 C T T T T A T A C T T T T A A G A C A A T T T T G G A G C C C C T C A C A G C C C T G C C T G C T 1800
Db 2653 C T T T T A T A C T T T T A A A G C A A T T T T T G G A G C C C C T C A C A G C C C T G C C T G C T 2712
Qy 1801 C A A C T A G C A G A T A C A G G A T A G G C A G C A C C T G A C T C T C T T A A G A G G C T G A G A G C C C A A A 1860
Db 2713 C A A C T A G C A G A T A C A G G A T A G G C A G C A C C T G A C T C T C T T A A G A G G C T G A G A G C C C A A A 2772
Qy 1861 C T G C T G T C C C A A A C A T G C A C T T C C T T G T T A A G T A T G G T A C A A G C A A T G C C T G C C C A A T 1920
Db 2773 C T G C T G T C C C A A A C A T G C A C T T C C T T G T T A A G G T A T G T A C A A G C A A T G C C T G C C C A A T 2832
Qy 1921 G G A G A A A A A C T T A A G T A G A T A A G A A A T A A G A C C A C T A T A A T T C T T C A C C T T A G G 1980
Db 2833 G G A G A A A A A C T T A A G T A G A T A A G A A A T A A G A A C C A C T A T A A T T C T T C A C C T T A G G 2892
Qy 1981 A A T A A T C C C T G T T A A T A T G T G T A C A T T C T T C C T G A T T A T T T C A C A C A T A C A T G T A A 2040
Db 2893 A A T A A T C C C T G T T A A T A T G T G T A C A T T C T C T G A T T A T T T C A C A C A T A C A T G T A A 2952
Qy 2041 A A T A T G C T T T T T T T T A A A T A G G G T T G T A C T A T G C T G T T A T A G T A G C C T T T A A T G A A T 2100
Db 2953 A A T A T G C T T T T T T T T A A A T A G G G T T G T A C T A T G C T G T T A T A G T A G C C T T T A A T G A A T 3012
Qy 2101 A A A C A T T T G T A G C A T C C T C T T T A A T G G G T A A C A G C 2136
Db 3013 A A A C A T T T G T A G C A T C C T C T T T A A T G G G T A A C A G C 3048
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RESULT 7

ID ADQ22926 standard; DNA; 2134 BP.

AC ADQ22926;

XX ADQ22926;

XX 26-AUG-2004 (first entry)

XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 5746.

DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;

XX ds.

XX Homo sapiens.

XX OS

XX WO2004048938-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US038193.

XX

PR 26-NOV-2002; 2002US-0429739P.
XX (PROT-) PROTEIN DESIGN LABS INC.
PA Aziz N, Ginsburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX Example 2; SEQ ID NO 5746; 210pp; English.
PS The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cyrostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC DNA of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX Sequence 2134 BP; 539 A; 586 C; 515 G; 494 T; 0 U; 0 Other;

Query Match 91.2%; Score 2061.6; DB 12; Length 2134;
Best Local Similarity 97.7%; Pred. No. 1.7e-280;
Matches 2130; Conservative 0; Mismatches 4; Indels 46; Gaps 2;
Qy 1 G A A T C A G G T C C G G G C G G C G A A G G G C G A A C T T T C C C C C C C G G C G C C C A C C G G C T 60
Db 1 G A A T C A G G T C C G G G C G G C G A A G G G C G A A C T T T C C C C C C C G G C G C C C A C C G G C T 60
Qy 61 C C C C G G G C C T C C C C T C G C G C C G A G C T T C G A G C A A G C A G C G T C C T G G G A G C G C G T C A 120
Db 61 C C C C G G G C C T C C C C T C G C G C C G A G C T T C G A G C A A G C A G C G T C C T G G G A G C G C G T C A 120
Qy 121 T G G C T T A C C A G T G A C C G C C T T G C T C T G C G C T G G C C T T G C T C C A C G C C C A G C G 180
Db 121 T G G C T T A C C A G C A C G C C T T G C T C C T G C G C T G G C C T T G C T C C A C G C C C A G C G 180
Qy 181 C G A G C A G T T C C G G G T G T C G C C G C T G G A T C G G A C C T G G A A C C T G G G C G A G A C A G T G G A G C 240
Db 181 C G A G C A G T T C C G G G T G T C G C C G C T G G A T C G G A C C T G G A A C C T G G G C G A G A C A G T G G A G C 240
Qy 241 T G A A G T C C A G G T G C T G T C C A A C C G A C G T G G G T G C T C G T G G T C T T T C C A G C G C G 300
Db 241 T G A A G T C C A G G T G C T G T C C A A C C G A C G T G G G T G C T C G T G G T C T T T C C A G C G C G 300
Qy 301 G C G C G C G C G C C A G T C C C A C C T T C C T A T A C T C T C C C A A A A A A A A G C C C A A G C G G G 360
Db 301 G C G C G C G C G C C A G T C C C A C C T T C C T A T A C T C T C C C A A A A A A A A G C C C A A G C G G G 360
Qy 361 C C G A G G G C T G G A C A C C A G C G G T T C T C G G G C A A G A G G T T G G G G A C A C C T T C G T C C T C A 420
Db 361 C C G A G G G C T G G A -----CA 375
Qy 421 C C C T G A G C G A C T T C C G C G A G A A C A G A G G G T A C T A T T T C T G C T C G G C C C T G A G C A A C T 480
Db 376 C C C T G A G C G A C T T C G C C G A G A A C A G A G G G T A C T A T T T C T G C T C G C C C T G A G C A A C T 435
Qy 481 C C A T C A T G T A C T T C A G C C A C T T C G T G C C G G T C T T C C T G C C A G C G A A G C C C A C C A C G A C G C 540
Db 436 C C A T C A T G T A C T T C A G C C A C T T C G T G C C G G T C T T C C T G C C A G C G A A G C C C A C C A G A C G C 495
Qy 541 C A G C G C G C G A C C A C C A C A C C G G C C C A C C A T C G C G T C G C A G C C C C T G T C C C T G C G C G C 600

| | | | |
|------|----|---|------|
| 496 | Db | CAGCGCCGCGACACACCAACACCGGGGCCCAACATCGCGTGCAGGCCCTGTCTCTCGCC | 555 |
| 601 | Qy | CAGAGCGGTGCGCGCCAGCGCGCGGGGCGCAGTGCACACAGAGGGGCTGCAGCTTCGCCCT | 660 |
| 556 | Db | CAGAGCGGTGCGCGCGACGCGCGGGGGCGCAGTGCACACGAGGGGCTGGACTTCGCCCT | 615 |
| 661 | Qy | GTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTCTGTCACTGG | 720 |
| 616 | Db | GTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTCTGTCACTGG | 675 |
| 721 | Qy | TTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCCCGGCCGTG | 780 |
| 676 | Db | TTATCACCCCTTTACTGCAACACAGGAACCGAAGACGTGTTGCAAAATGTCCCGGCCGTG | 735 |
| 781 | Qy | TGGTCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 840 |
| 736 | Db | TGGTCAAAATCGGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTCTAAACCTGTGCAACAG | 795 |
| 841 | Qy | CCACTACATTACTTCAAACTGAGATCTCTTCTTTTGGGGAGCAAGTCTCTTCCCTTTTCAT | 900 |
| 796 | Db | CCACTACATTACTTCAAACTGAGATCTCTTCTTTTGGGGAGCAAGTCTCTTCCCTTTTCAT | 855 |
| 901 | Qy | TTTTTTCAGACTCTTCCCTCCCTGTGTATTCATTTCTCATGATTTATTTTACTGTGGGGGGG | 960 |
| 856 | Db | TTTTTTCAGACTCTTCCCTCCCTGTGTATTCATTTCTCATGATTTATTTTACTGTGGGGGGG | 915 |
| 961 | Qy | GTGGAAAGATTACTTTTTTCTTATGTGTGTTGACGGGAAACAAAACTAGTGTAAAATCTAC | 1020 |
| 916 | Db | GTGGAAAGATTACTTTTTTCTTATGTGTGTTGACGGGAAACAAAACTAGTGTAAAATCTAC | 975 |
| 1021 | Qy | AGTACACACAAGGGTCACAATACGTGTGTGCGCACATCGCGGTAGGCGTGTGAAAGGGG | 1080 |
| 976 | Db | AGTACACACAAGGGTCACAATACGTGTGTGCGCACATCGCGGTAGGCGTGTGAAAGGGG | 1035 |
| 1081 | Qy | CAGCCAGAGCTACCCGACAGTCTCAGAAATCATGCTGAGAGAGCTGTGAGGCGACCCATG | 1140 |
| 1036 | Db | CAGCCAGAGCTACCCGACAGTCTCAGAAATCATGCTGAGAGAGCTGTGAGGCGACCCATG | 1095 |
| 1141 | Qy | CCATCTCAAACTCTTCCCGCCCGCTTTTACAAGGGGGAGGCTTAAAGCCACAGAGACAGCT | 1200 |
| 1096 | Db | CCATCTCAAACTCTTCCCGCCCGCTTTTACAAGGGGGAGGCTTAAAGCCACAGAGACAGCT | 1155 |
| 1201 | Qy | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1260 |
| 1156 | Db | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGACCTTGTCTCCCA | 1215 |
| 1261 | Qy | GCTCAGGCGCTTTCCTCCACACCAATTCAGTCTTCTTTCGAGGGCCCTGTCTCAGGG | 1320 |
| 1216 | Db | GCTCAGGCGCTTTCCTCCACACCAATTCAGTCTTCTTTCGAGGGCCCTGTCTCAGGG | 1275 |
| 1321 | Qy | TGAGGTGCTTGAGTCTCCACGGCAAGGAAACAGTACTCTTGTATACCTGGGATACTGT | 1380 |
| 1276 | Db | TGAGGTGCTTGAGTCTCCACGGCAAGGAAACAGTACTCTTGTATACCTGGGATACTGT | 1335 |
| 1381 | Qy | GCCCAGAGCCTCGAGGAGTAAATGAAATTAAGAGAGAACTGCGCTTTGGCAGAGTCTCAT | 1440 |
| 1336 | Db | GCCCAGAGCCTCGAGGAGTAAATGAAATTAAGAGAGAACTGCGCTTTGGCAGAGTCTCAT | 1395 |
| 1441 | Qy | AATGTAAACAAATATCAGACTTTTTTTTTTTTATTAATCAAGGCTTAAATGTATGAGACTAA | 1500 |
| 1396 | Db | AATGTAAACAAATATCAGAC-TTTTTTTTTTTTATTAATCAAGGCTTAAATGTATGAGACTAA | 1454 |
| 1501 | Qy | AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTACTCTTAAGAAAT | 1560 |
| 1455 | Db | AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTACTCTTAAGAAAT | 1514 |
| 1561 | Qy | CTCTGTGAAACCCCTATGTGAGGCGGAAATTGCTCTCCAGCCCTTGCAATTCAGAGGGG | 1620 |
| 1515 | Db | CTCTGTGAAACCCCTATGTGAGGCGGAAATTGCTCTCCAGCCCTTGCAATTCAGAGGGG | 1574 |
| 1621 | Qy | CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGACTCATGAGGTTAAA | 1680 |
| 1575 | Db | CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGACTCATGAGGTTAAA | 1634 |

| | | | |
|----------|-------------|---|------|
| QY | 1681 | CTAAGGCCCTCTGAAATCTCTGAAATTGGAGATACAAACATGTTCCTGGGGAATCACTGATGA | 1740 |
| Db | 1635 | CTAAGGCCCTCTTGAATCTCTGAAATTGGAGATACAAACATGTTCCTGGGATCACTGATGA | 1694 |
| QY | 1741 | CTTTTTATACTTTTGTAAGAACAATTGTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT | 1800 |
| Db | 1695 | CTTTTTATACTTTTGTAAGAACAATTGTTGAGAGGCCCTCACACAGCCCTGGCCTCTGCT | 1754 |
| QY | 1801 | CAACTAGCAGATACAGGGATGAGGCAGACCTGACTCTCTTTAAGGAGGCTGAGAGCCCCAAA | 1860 |
| Db | 1755 | CAACTAGCAGATACAGGGATGAGGCAGACCTGACTCTCTTTAAGGAGGCTGAGAGCCCCAAA | 1814 |
| QY | 1861 | CTGCTGTCCCACACATGCATCTTCCTTGCTTTAAGGTATGGTACAAGCATGCGCTGCCCAATT | 1920 |
| Db | 1815 | CTGCTGTCCCACACATGCATCTTCCTTGCTTTAAGGTATGGTACAAGCATGCGCTGCCCAATT | 1874 |
| QY | 1921 | GGAGAGAAAAAACCTTTAAGTAGATAAGGAAATAAGAACCCACTCATTAATTTCTACCTTTAGG | 1980 |
| Db | 1875 | GGAGAGAAAAAACCTTTAAGTAGATAAGGAAATAAGAACCCACTCATTAATTTCTACCTTTAGG | 1934 |
| QY | 1981 | AATAAATCTCCTGTTAATPATCGGTGTACATCTTCTCTGATTAATTTTCTACACATACATGTAA | 2040 |
| Db | 1935 | AATAAATCTCCTGTTAATPATCGGTGTACATCTTCTCTGATTAATTTTCTACACATACATGTAA | 1994 |
| QY | 2041 | AATATGTCCTTCTTTTAAATAGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT | 2100 |
| Db | 1995 | AATATGTCCTTCTTTTAAATAGGTTGTACTATGCTGTTATGAGTGGCTTTAATGAAT | 2054 |
| QY | 2101 | AAACATTTGTAGATCCTCTTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2160 |
| Db | 2055 | AAACATTTGTAGATCCTCTTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAA | 2114 |
| QY | 2161 | AAAAAAAAAAAAAAAAAAAAA 2180 | |
| Db | 2115 | AAAAAAAAAAAAAAAAAAAAA 2134 | |
| RESULT 8 | | | |
| ADF90782 | | | |
| ID | ADF90782 | standard; DNA; 2123 BP. | |
| XX | ADF90782; | | |
| AC | | | |
| XX | | | |
| DT | 26-FEB-2004 | (first entry) | |
| XX | | | |
| DE | | Human hepatic-fibrosis disease marker SEQ ID 244. | |
| XX | | | |
| KW | | Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis; | |
| KW | | hepatic carcinoma; human; ds. | |
| XX | | | |
| OS | | Homo sapiens. | |
| XX | | | |
| PN | | JP2003259877-A. | |
| XX | | | |
| PD | | 16-SEP-2003. | |
| XX | | | |
| PF | | 11-MAR-2002; 2002JP-00065013. | |
| XX | | | |
| PR | | 11-MAR-2002; 2002JP-00065013. | |
| XX | | | |
| PA | | (SUMU) SUMITOMO SEIYAKU KK. | |
| XX | | | |
| DR | | WPI; 2003-821598/77. | |
| XX | | | |
| PT | | Hepatic fibrosis disease markers comprising polynucleotides or | |
| PT | | antibodies, useful for improved diagnosis, screening and developing drugs | |
| PT | | to treat hepatitis, to control cirrhosis and carcinoma. | |
| XX | | | |
| PS | | Claim 1; SEQ ID NO 244; 313pp; Japanese. | |
| XX | | | |
| CC | | The present invention relates to hepatic-fibrosis disease markers | |
| CC | | (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The | |

db 1984 CTACACATACATGTAAATATGTCCTTCTTTTAAATAGGGTTGTACTATGCTGTATG 2043

QY 2085 AGTGGCTTTAATGAATAAACATTTGTAGCATCCTCTTTAA 2124

Db
2044 AGTGGCTTTTAAATGAATAAACAATTGTAGCATCCTCCTAAA 2083

RESULT 9
AD002702

| ID | ADS92793 standard; cDNA; 2150 BP. |
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| 11 | 11 |
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| 95 | 95 |
| 96 | 96 |
| 97 | 97 |
| 98 | 98 |
| 99 | 99 |
| 100 | 100 |

AA
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ADS92793;

XX
DT 16-DEC-20XX
DE
XX

XX
XXXXX OF A GROUP CONCERN ALTERNATIVE TRANSCRIPTION.

KW immune response; cell-specific antigen; alloantigen; CD8;
KW CD8 alpha-chain; cellular immune response; humoral immune response;

KW transplant allograft; graft-versus-host disease; transplant; gene; ss.
 XX

OS Homo sapiens.

| Key | Location/Qualifiers |
|-----|---------------------|
| AA | |
| FH | |

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CDS
FT 120.716
FT /*tag= a

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FT yy /product= "CD8 alpha-chain"
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PN WO2004083244-A2.

30-SEP-2004.

XX
PF
19-MAR-2004:

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12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, PA (TSOG-) ISOGENIS INC.
XX

PI Qi Y, Zhang X, Konigsberg PJ;
XX

DR WPI; 2004-691022/67.

[illegible]

PT e.g. treating graft-versus-host disease: comprises contacting a target specifically inhibiting host immune responses to alloantigens, useful for

PT cell expressing the antigen with an expression vector encoding a CD8 polypeptide

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| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 | 101 | 102 | 103 | 104 | 105 | 106 | 107 | 108 | 109 | 110 | 111 | 112 | 113 | 114 | 115 | 116 | 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 | 301 | 302 | 303 | 304 | 305 | 306 | 307 | 308 | 309 | 310 | 311 | 312 | 313 | 314 | 315 | 316 | 317 | 318 | 319 | 320 | 321 | 322 | 323 | 324 | 325 | 326 | 327 | 328 | 329 | 330 | 331 | 332 | 333 | 334 | 335 | 336 | 337 | 338 | 339 | 340 | 341 | 342 | 343 | 344 | 345 | 346 | 347 | 348 | 349 | 350 | 351 | 352 | 353 | 354 | 355 | 356 | 357 | 358 | 359 | 360 | 361 | 362 | 363 | 364 | 365 | 366 | 367 | 368 | 369 | 370 | 371 | 372 | 373 | 374 | 375 | 376 | 377 | 378 | 379 | 380 | 381 | 382 | 383 | 384 | 385 | 386 | 387 | 388 | 389 | 390 | 391 | 392 | 393 | 394 | 395 | 396 | 397 | 398 | 399 | 400 | 401 | 402 | 403 | 404 | 405 | 406 | 407 | 408 | 409 | 410 | 411 | 412 | 413 | 414 | 415 | 416 | 417 | 418 | 419 | 420 | 421 | 422 | 423 | 424 | 425 | 426 | 427 | 428 | 429 | 430 | 431 | 432 | 433 | 434 | 435 | 436 | 437 | 438 | 439 | 440 | 441 | 442 | 443 | 444 | 445 | 446 | 447 | 448 | 449 | 450 | 451 | 452 | 453 | 454 | 455 | 456 | 457 | 458 | 459 | 460 | 461 | 462 | 463 | 464 | 465 | 466 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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The specification describes a method for specifically inhibiting a host immune response to target cell-specific antigens (e.g. alloantigens). The method comprises contacting a target cell expressing the antigen with an expression vector encoding a CD8 polypeptide comprising the CD8 alpha-chain, where the CD8 polypeptide is expressed by the target cell and where the host immune response against the target cell is specifically inhibited. The method of the invention is useful for specifically inhibiting both cellular and humoral immune responses to alloantigens, thus finding use in extending the survival of transplant allografts and in treating graft-versus-host disease in transplant recipients. The present sequence encodes an alternative transcript of a secreted alpha-chain of a CD8 protein. This CD8 alpha-chain may be used in the method of the invention.

SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

Query Match 89.7%; Score 2029; DB 13; Length 2150;

Matches 2150; Conservative 0; Mismatches 0; Indels 111;

QY 1 GAAATCAGGCTCCGGGCCGGCCGAAGGGCGCAACTTTCCCCCTCGGGCGCCCA CCGGCT 60

bp
1 GAATCAGGCTCCGGCGCGCAAGCGCCCAATTTCACCGCCGCCGCCTTCCCC

| | | | |
|----|------|---|------|
| QY | 61 | CCGCGCGGCTCCCTCGGCGCCGAGCTTCGAGCCACAGAGCGTCTCTGGGAGCGCGTCA | 120 |
| DB | 61 | CCGCGCGGCTCCCTCGGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCTGGGAGCGCGTCA | 120 |
| QY | 121 | TGGCCCTTACCACTGACCGCTTGCTCTGCGCGCTGGCCCTTGCTCTCCACAGCGCCGAGCG | 180 |
| DB | 121 | TGGCCCTTACCACTGACCGCTTGCTCTGCGCGCTGGCCCTTGCTCTCCAGCGCGCCAGCG | 180 |
| QY | 181 | CGAGCCAGTTCCGGGTGTGCGCGCTGGAATCGGAACCTGGGCGGAGACAGTGGAGC | 240 |
| DB | 181 | CGAGCCAGTTCCGGGTGTGCGCGCTGGAATCGGAACCTGGGCGGAGACAGTGGAGC | 240 |
| QY | 241 | TGAAGTGCACAGTGTCTGTCTCAACCCGAGCTGGGCTGTCTGCGGCTCTTCCACGCCG | 300 |
| DB | 241 | TGAAGTGCACAGTGTCTGTCTCAACCCGAGCTGGGCTGTCTGCGGCTCTTCCACGCCG | 300 |
| QY | 301 | GCGGCGCGCGCCAGTCCACCTTCCTCTATAGCTCTCCCAAAACAGGCCAACAGGCGG | 360 |
| DB | 301 | GCGGCGCGCGCCAGTCCACCTTCCTCTATAGCTCTCCCAAAACAGGCCAACAGGCGG | 360 |
| QY | 361 | CCGAGGGGCTGGAACACCCAGCGGTTCTCGGCAAGAGTGTGGGGACACCTTCGCTCTCA | 420 |
| DB | 361 | CCGAGGGGCTGGAACACCCAGCGGTTCTCGGCAAGAGTGTGGGGACACCTTCGCTCTCA | 420 |
| QY | 421 | CCCTGAGCGACTTCGCGCGAGAAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAACT | 480 |
| DB | 421 | CCCTGAGCGACTTCGCGCGAGAAACGAGGGCTACTATTTCTGCTCGGCCCTTGAGCAACT | 480 |
| QY | 481 | CCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCGCGAGGAAGCCACACGAGCGC | 540 |
| DB | 481 | CCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCGCGAGGAAGCCACACGAGCGC | 540 |
| QY | 541 | CAGCGCCGCGACCAACACCGCGGCCCAACCATCGCGTTCGAGCGCCCTGTCCCTGCGCGC | 600 |
| DB | 541 | CAGCGCCGCGACCAACACCGCGGCCCAACCATCGCGTTCGAGCGCCCTGTCCCTGCGCGC | 600 |
| QY | 601 | CAGAGCGTGTGCGGCGAGCGGGGGGCGCAGTGCAACAGAGGGGGCTGGACTTCGCCCT | 660 |
| DB | 601 | CAGAGCGTGTGCGGCGAGCGGGGGGCGCAGTGCAACAGAGGGGGCTGGACTTCGCCCT | 660 |
| QY | 661 | GTGATATCTACATCTGGSGCGCCCTTGGCGGAGCTTGTGGGGTCCCTCTCTGTCTCACTGG | 720 |
| DB | 634 | ----- | 633 |
| QY | 721 | TTATCAACCTTTTACGTCAACACAGGAAACCGAAGACGTGTTTGCAAAATGTCCTCCGCGCTG | 780 |
| DB | 634 | -----GGAAACCGAAGACGTGTTTGCAAAATGTCCTCCGCGCTG | 669 |
| QY | 781 | TGTCCTAAATCGGGAGACAGCCCGAGCTTTTCGGCGAGATAGTCTAAACCTGTGTGCAACAG | 840 |
| DB | 670 | TGTCCTAAATCGGGAGACAGCCCGAGCTTTTCGGCGAGATAGTCTAAACCTGTGTGCAACAG | 729 |
| QY | 841 | CCACTACATTAATCTCAAACTCAGATCTCTCTTTTGGAGGAGCAAGTCTCTTCCCTTTTCAT | 900 |
| DB | 730 | CCACTACATTAATCTCAAACTCAGATCTCTCTTTTGGAGGAGCAAGTCTCTTCCCTTTTCAT | 789 |
| QY | 901 | TTTTTCCAGTCTCCTCCCTGTATTCATTTCTCATGATTAATATTTTAGTGGGGCGGG | 960 |
| DB | 790 | TTTTTCCAGTCTCCTCCCTGTATTCATTTCTCATGATTAATATTTTAGTGGGGCGGG | 849 |
| QY | 961 | GTGGGAAAGATTAATTTTTTTTATGTGTTTGGAGGGGAAACAAACTAGGTAATAATCTAC | 1020 |
| DB | 850 | GTGGGAAAGATTAATTTTTTTTATGTGTTTGGAGGGGAAACAAACTAGGTAATAATCTAC | 909 |
| QY | 1021 | AGTACACCAAGGGTCAACATCTGTGTGCGCACATCGCGGTAGGCGCTGGAAAGGGG | 1080 |
| DB | 910 | AGTACACCAAGGGTCAACATCTGTGTGCGCACATCGCGGTAGGCGCTGGAAAGGGG | 969 |
| QY | 1081 | CAGGCCAGAGCTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGCACCCCATG | 1140 |
| DB | 970 | CAGGCCAGAGCTACCCGCGAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGCACCCCATG | 1020 |

QY 1141 CCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCAGACAGCT 1200
Db |||||
QY 1030 CCATCTCAACCTCTTCCCGCCCGCTTTTACAAAGGGGAGGCTAAAGCCAGACAGCT 1089
Db |||||
QY 1201 TGATCAAAAGGCACACAGCAAGCTCAGGGTGTGAGCAGTAGCTGAGGGACCTTGTCTCCCA 1260
Db |||||
QY 1090 TGATCAAAAGGCACACAGCAAGCTCAGGGTGTGAGCAGTAGCTGAGGGACCTTGTCTCCCA 1149
Db |||||
QY 1261 GCTCAGGCTCTTCTCTCCACACCATTCAGTCTTCTTTCCGAGGCCCTGTCTCAGGG 1320
Db |||||
QY 1150 GCTCAGGCTCTTCTCTCCACACCATTCAGTCTTCTTTCCGAGGCCCTGTCTCAGGG 1209
Db |||||
QY 1321 TGAGTCTTCTGAGTCTCCAAAGGCAAGGACAGTACTTCTTATACCTGGGATCTGT 1380
Db |||||
QY 1210 TGAGTCTTCTGAGTCTCCAAAGGCAAGGACAGTACTTCTTATACCTGGGATCTGT 1269
Db |||||
QY 1381 GCCCAGAGCTCGAGGAGGTAAATGAATTAAGAGAGAGAACTGCCTTTTGGCAGAGTCTAT 1440
Db |||||
QY 1270 GCCCAGAGCTCGAGGAGGTAAATGAATTAAGAGAGAGAACTGCCTTTTGGCAGAGTCTAT 1329
Db |||||
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCCTAAATTTGTATAGACTTAA 1500
Db |||||
QY 1330 AATGTAAACAATATCAGACTTTTTTTTTTTTATAATCAAGCCCTAAATTTGTATAGACTTAA 1389
Db |||||
QY 1501 AATAAATGAAGTGTGAGCTTAACCTTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db |||||
QY 1390 AATAAATGAAGTGTGAGCTTAACCTTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1449
Db |||||
QY 1561 CTCTGTGAAACCCCTATCTGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTTGCAGAGGG 1620
Db |||||
QY 1450 CTCTGTGAAACCCCTATCTGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTTGCAGAGGG 1509
Db |||||
QY 1621 CCCATGAAGAGGACAGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db |||||
QY 1510 CCCATGAAGAGGACAGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1569
Db |||||
QY 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGATCAGTGATGA 1740
Db |||||
QY 1570 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTGGATCAGTGATGA 1629
Db |||||
QY 1741 CTTTATTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACACAGCCCTGGCCTCTGCT 1800
Db |||||
QY 1630 CTTTATTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACACAGCCCTGGCCTCTGCT 1689
Db |||||
QY 1801 CAACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTTAAGGAGGTGAGAGCCCAA 1860
Db |||||
QY 1690 CAACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTTAAGGAGGTGAGAGCCCAA 1749
Db |||||
QY 1861 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGATGATCAAGCAATGCTGCCCCATT 1920
Db |||||
QY 1750 CTGCTGTCCCAACATGCACTCTCTTCTTAAAGTATGATGATCAAGCAATGCTGCCCCATT 1809
Db |||||
QY 1921 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1980
Db |||||
QY 1810 GGAGAGAAAAAATTTAAGTAGATAAGGAAATAGAACCACTCATATTTCTTCACTTAGG 1869
Db |||||
QY 1981 AATATCTCTGTTAATATGTTGATCACTTCTTCTGATTTATTTCTACACATACATGTA 2040
Db |||||
QY 1870 AATATCTCTGTTAATATGTTGATCACTTCTTCTGATTTATTTCTACACATACATGTA 1929
Db |||||
QY 2041 AATATCTCTTCTTTTAAATAGGTTGATGATGCTGTTATGATGCTGCTTTATGAT 2100
Db |||||
QY 1930 AATATCTCTTCTTTTAAATAGGTTGATGATGCTGTTATGATGCTGCTTTATGAT 1989
Db |||||
QY 2101 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAGCAAGCAAAAAAATTTTTTTTTTAAAA 2160
Db |||||
QY 1990 AAACATTTGTAGCATCTCTTTTAAATAGGTTAAGCAAGCAAAAAAATTTTTTTTTTAAAA 2049
Db |||||
QY 2161 AAAAAAATT 2220
Db |||||
QY 2050 AAAAAAATT 2109
Db |||||
QY 2221 AAAAAAATT 2261
Db |||||

Db |||||
2110 AA 2150
RESULT 10
ADSI9439
ID ADS19439 standard; DNA; 2150 BP.
XX ADS19439;
AC ADS19439;
XX 16-DEC-2004 (first entry)
DT
XX Human secreted protein related to CD8 alpha chain DNA.
DE
XX human; gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 120..716
FT /*tag= a
FT /product= "CD8 alpha chain related protein"
XX
PN WO2004083404-A2.
XX
XX 30-SEP-2004.
XX
XX 19-MAR-2004; 2004WO-US008567.
XX
XX 19-MAR-2003; 2003US-0456378P.
XX
XX (ISOG-) ISOGENIS INC.
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XX Qi Y, Zhang X, Konigsberg PJ;
XX
XX WPI; 2004-691049/67.
DR P-PSDB; ADS19438.
XX
XX
PT New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
operably linked to a nucleic acid encoding a transmembrane polypeptide,
useful for inhibiting cellular and humoral components of the host immune
responses.
XX
PS Disclosure; Fig 1; 94pp; English.
XX
CC This invention relates to novel gene therapy vectors with reduced
immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
alpha chain operably linked to nucleic acid encoding a transmembrane
polypeptide and a second nucleic acid representing the therapeutic gene
of interest (for example ornithine carbamoyl transferase or beta
glucosidase), whereby transcriptional and translational control elements
direct expression thereof. The present invention describes a method to
reduce an immune response against antigens derived from a gene therapy
delivery system i.e. improving the expression of a therapeutic transgene
in a host and improving viral expression vectors with reduced
immunogenicity. Accordingly, these compositions are useful for inhibiting
both the cellular and humoral components of the host immune responses
against expression vectors and target cells transfected with the vectors.
CC As such, they exhibit immunosuppressive activity. This polynucleotide is
the DNA sequence of a human secreted protein (derived from an alternate
transcript) related to the CD8 alpha chain of the invention.
XX
SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;
Query Match 89.7%; Score 2029; DB 13; Length 2150;
Best Local Similarity 95.1%; Pred. No. 6.5e-276;
Matches 2150; Conservative 0; Mismatches 0; Indels 11; Gaps 1;
QY 1 GAAATCAGGCTCCGGGCGCGGCGAAGGGCGCAACTTTCCCTCCCTCGGCGCCACCGGCT 60
Db 1 GAAATCAGGCTCCGGGCGCGGCGAAGGGCGCAACTTTCCCTCCCTCGGCGCCACCGGCT 60

QY 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCAAGACGCTCTGGGGAGCGCTCA 120
Db 61 CCCGCGCGCTCCCTCGCGCCGAGCTTCGAGCAAGACGCTCTGGGGAGCGCTCA 120
QY 121 TGGCTTTACAGTGAACCGCTTGTCTGCTCGCGCTGGCTTGTCTGCTCCACGCGCGCAGGC 180
Db 121 TGGCTTTACAGTGAACCGCTTGTCTGCTCGCGCTGGCTTGTCTGCTCCACGCGCGCAGGC 180
QY 181 CGAGCCAGTTTCGGGTGTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTTCGGGTGTCGCGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAGC 240
QY 241 TGAAGTGCAGAGTGTCTGCTCAACCCGAGCTCGGGCTGCTGCTGCTTTCAGCCGC 300
Db 241 TGAAGTGCAGAGTGTCTGCTCAACCCGAGCTCGGGCTGCTGCTGCTTTCAGCCGC 300
QY 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 360
Db 301 GCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 360
QY 361 CGAGGGGCTGAGACACCCAGCGTTCTCGGCGAAGAGTTGGGGACACCTTCGTCTCTCA 420
Db 361 CGAGGGGCTGAGACACCCAGCGTTCTCGGCGAAGAGTTGGGGACACCTTCGTCTCTCA 420
QY 421 CCTGAGCGCACTTCCGCGAGAGAACGAGGGCTACTATTTCCTGCTGGGCCCTGAGCAACT 480
Db 421 CCTGAGCGCACTTCCGCGAGAGAACGAGGGCTACTATTTCCTGCTGGGCCCTGAGCAACT 480
QY 481 CCATCATGTACTTCAGCACTTCGTGCGGTCTTCCTGCGAGCAAGCCCAACGACGC 540
Db 481 CCATCATGTACTTCAGCACTTCGTGCGGTCTTCCTGCGAGCAAGCCCAACGACGC 540
QY 541 CAGCGCGCGGACCAACCAACCGCGCCCAACCATCGCTGCGAGCCCTGTCTCGGCC 600
Db 541 CAGCGCGCGGACCAACCAACCGCGCCCAACCATCGCTGCGAGCCCTGTCTCGGCC 600
QY 601 CAGAGCGTCCGCGCAGCGCGGGGGCGAGTGCACAGAGGGGCTGGACTTCGCCT 660
Db 601 CAGAGCGTCCGCGCAGCGCGGGGGCGAG- 633
QY 661 GTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCCTGCTACTGG 720
Db 634 ----- 633
QY 721 TTATCACCTTTACTGCAACCAAGGAACCGAGAGCTGTTTGCAAAATGTCCCGGCGCTG 780
Db 634 -----GGAA CCGAAGACGTGTGTGCAAAATGTCCCGGCGCTG 669
QY 781 TGGTCAAAATCGGAGACAAAGCCAGCCTTTCGCGAGATACGCTTAAACCTGTGCAACAG 840
Db 670 TGGTCAAAATCGGAGACAAAGCCAGCCTTTCGCGAGATACGCTTAAACCTGTGCAACAG 729
QY 841 CCACTACATTTACTTCAAACTGAGATCCTTCTTTGAGGGAGCAAGTCTTCCCTTTTCA 900
Db 730 CCACTACATTTACTTCAAACTGAGATCCTTCTTTGAGGGAGCAAGTCTTCCCTTTTCA 789
QY 901 TTTTTCAGTCTTCTCCCTGTGTTTCAATCTCATGATTATTATTTAGTGGGGCGGG 960
Db 790 TTTTTCAGTCTTCTCCCTGTGTTTCAATCTCATGATTATTATTTAGTGGGGCGGG 849
QY 961 GTGGGGAAGATTACTTTTTTCTTTATGTGTTTGAACGGGAAACAACTAGGTAAATCTAC 1020
Db 850 GTGGGGAAGATTACTTTTTTCTTTATGTGTTTGAACGGGAAACAACTAGGTAAATCTAC 909
QY 1021 AGTACACCAAGAGGTCAAACTACTGTTGTCGCACATCGCGTAGGGCTGGAAAGGGG 1080
Db 910 AGTACACCAAGAGGTCAAACTACTGTTGTCGCACATCGCGTAGGGCTGGAAAGGGG 969
QY 1081 CAGGGCCAGAGCTACCGCGAGAGTCTCAGAAATCATGCTCAGAGAGCTGGAGGCACCCATG 1140
Db 970 CAGGGCCAGAGCTACCGCGAGAGTCTCAGAAATCATGCTCAGAGAGCTGGAGGCACCCATG 1029
QY 1141 CCATCTCAACCTCTTCCCGCGCGCTTTTACAAGGGGAGGCTAAAGCCCGAGAGACAGCT 1200

Db 1030 CCATCTCAACCTCTTCCCGCGCGCTTTTACAAGGGGAGGCTAAAGCCCGAGAGACAGCT 1089
QY 1201 TGATCAAAAGCCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1260
Db 1090 TGATCAAAAGCCACACAGCAAGTCAAGGTTCGAGCAGTAGCTGGAGGACCTTGTCTCCCA 1149
QY 1261 GCTCAGGGCTCTTTTCCCTCCACACATTCAGGTCTTTTCCGAGGGCCCTGTCTCAGGG 1320
Db 1150 GCTCAGGGCTCTTTTCCCTCCACACATTCAGGTCTTTTCCGAGGGCCCTGTCTCAGGG 1209
QY 1321 TGAGGTGCTTGAGTCTCCAAACGGGAAAGGAACTTCTTCTGATACCTTGGGAACTACTGT 1380
Db 1210 TGAGGTGCTTGAGTCTCCAAACGGGAAAGGAACTTCTTCTGATACCTTGGGAACTACTGT 1269
QY 1381 GCCCAGAGCTCCGAGGAGGTAAATGAATTAAGAGAGAACTGCTTTTGGCAGAGTTCTAT 1440
Db 1270 GCCCAGAGCTCCGAGGAGGTAAATGAATTAAGAGAGAACTGCTTTTGGCAGAGTTCTAT 1329
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1500
Db 1330 AATGTAAACAATATCAGACTTTTTTTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1389
QY 1501 AATAAATGAAGTGTGAGCTTAAACCTTGGAATGAATCCCTCTATCTCTAAAGAAAAAT 1560
Db 1390 AATAAATGAAGTGTGAGCTTAAACCTTGGAATGAATCCCTCTATCTCTAAAGAAAAAT 1449
QY 1561 CTCTGTGAAACCCCTATGTGGAGCGGAATTTGCTCTCCAGGCCCTTGCATTTGCAGAGGG 1620
Db 1450 CTCTGTGAAACCCCTATGTGGAGCGGAATTTGCTCTCCAGGCCCTTGCATTTGCAGAGGG 1509
QY 1621 CCCATGAAGAGAGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1680
Db 1510 CCCATGAAGAGAGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1569
QY 1681 CTAAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTTCTGGGATCACTGATGA 1740
Db 1570 CTAAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTTCTGGGATCACTGATGA 1629
QY 1741 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCAACAGCCCTTGGCTCTGCT 1800
Db 1630 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCAACAGCCCTTGGCTCTGCT 1689
QY 1801 CAACTAGCAGATACAGGGATGAGGACGCTGACTCTCTTTAAGGAGGCTGAGAGGCCAAA 1860
Db 1690 CAACTAGCAGATACAGGGATGAGGAGCAGCTGACTCTCTTTAAGGAGGCTGAGAGGCCAAA 1749
QY 1861 CTGCTGTCCCAACATGCACTTCTTGTAAAGGTATGTTAAGCAATGCTTGCCTTGCCTT 1920
Db 1750 CTGCTGTCCCAACATGCACTTCTTGTAAAGGTATGTTAAGCAATGCTTGCCTTGCCTT 1809
QY 1921 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATTAATTTCTACCTTAGG 1980
Db 1810 GGAGAGAAAAAATTAAGTAGATAGGAATTAAGAACCACTCATTAATTTCTACCTTAGG 1869
QY 1981 AATAATCTCCTGTTAATAGGTGATCATTTCTTCTGATTATTTTCTACACATCATGTA 2040
Db 1870 AATAATCTCCTGTTAATAGGTGATCATTTCTTCTGATTATTTTCTACACATCATGTA 1929
QY 2041 AATAATCTCCTTTTAAATPAGGGTGTACTATGCTTATGAGTGGCTTTTAAATGAAT 2100
Db 1930 AATAATCTCCTTTTAAATPAGGGTGTACTATGCTTATGAGTGGCTTTTAAATGAAT 1989
QY 2101 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCAAAAAAAGAAAAAAGAAAAA 2160
Db 1990 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCAAAAAAAGAAAAAAGAAAAA 2049
QY 2161 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2220
Db 2050 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2109
QY 2221 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 2261

1270 G C C C A G A G C C T C G A G G A G T A A T G A A T T A A G A G A G A A C T G C C T T T G G C A G A G T T C T A T 1329
1441 A A T G T A A A C A A T A T C A G A C T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 1500
1330 A A T G T A A A C A A T A T C A G A C T T T T T T T T T T A T A A T C A A G C C T A A A A T T G T A T A G A C C T A A 1389
1501 A A T A A A T G A A G T G T G A G C T T A A C C C T G G A A A T G A A T C C C T C T A T C T A A G A A A A T 1560
1390 A A T A A A T G A A G T G T G A G C T T A A C C C T G G A A A T G A A T C C C T C T A T C T A A G A A A T 1449
1561 C T C T G T A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1620
1450 C T C T G T A A C C C T A T G T G A G G C G G A A T T G C T C C C A G C C C T T G C A T T G C A G A G G G 1509
1621 C C C A T G A A A G A G A C A G G C T A C C C C T T T A C A A T A G A A T T T G A G C A T C A G T A G G T T A A 1680
1510 C C C A T G A A A G A G A C A G G C T A C C C C T T T A C A A T A G A A T T T G A G C A T C A G T A G G T T A A 1569
1681 C T A A G C C C T T T G A A T C T G A A T T T G A T A C A A A C A T G T T C T G G A T C A C T G A T G A 1740
1570 C T A A G C C C T T T G A A T C T G A A T T T G A T A C A A A C A T G T T C C T G G A T C A C T G A T G A 1629
1741 C T T T T A T A C T T T G T A A G A C A A T T T T G A G A G C C C C T C A C A G C C C T G C C T T G C T 1800
1630 C T T T T A T A C T T T G T A A G A C A A T T T T G A G A G C C C C T C A C A G C C C T G C C T T G C T 1689
1801 C A A T A G A C A T A C A G G A T A G G C A G C T C A C T C T T T A A G A G G C T G A G A G C C A A 1860
1690 C A A T A G A C A T A C A G G A T A G G C A G C T C A C T C T T T A A G A G G C T G A G A G C C A A 1749
1861 C T G C T G T C C C A A C A T G C A C T T C C T T G T T A A G T A T G T A C A A G C A A T G C C T G C C A T T 1920
1750 C T G C T G T C C C A A C A T G C A C T T C C T T G C T T A A G T A T G T A C A A G C A A T G C C T G C C A T T 1809
1921 G A G A G A A A A A C T T A A G T A G A T A G A A A T A A G A A C C A C T C A T A A T T C C T C A C C T T A G G 1980
1810 G G A G A G A A A A C T T A A G T A G A T A A G G A A T A A G A A C C A C T C A T A A T T C C A C C T T A G G 1869
1981 A A T A A T C T C T G T T A A T A T G T G T A C A T T C T C C T G A T T A T T T C T A C A C A T A C A T G T A A 2040
1870 A A T A A T C T C C T G T T A A T A T G T G T A C A T T C T C C T G A T T A T T T C T A C A C A T A C A T G T A A 1929
2041 A A T A T G T C T T C T T T T T A A A T A G G T T G T A C T A T G T A T G A T G G C T T T A A T G A A T 2100
1930 A A T A T G T C T T C T T T T T A A A T A G G T T G T A C T A T G C T G T A T G A T G C T T T A A T G A A T 1989
2101 A A A C A T T T G T A C A T C C T T T T A A T G G T A A C A G C A 2160
1990 A A A C A T T T G T A C A T C C T T T T A A T G G T A A A C A G C A 2049
2161 A 2220
2050 A 2109
2221 A 2261
2110 A 2150

RESULT 12
AED96282
ID AED96282 standard; DNA; 3518 BP.
XX AC AED96282;
XX DT 26-JAN-2006 (first entry)
XX DE Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 439.
XX KW Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;

KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
KW C-reactive protein pentraxin-related; CRP; Genetic marker; ds.
XX OS Homo sapiens.
XX PN WO2005107364-A2.
XX PD 17-NOV-2005.
XX PF 27-JAN-2005; 2005WO-IB002407.
XX PR 27-JAN-2004; 2004US-0539128P.
PR 27-JAN-2004; 2004US-0539129P.
PR 22-OCT-2004; 2004US-0620874P.
PR 22-OCT-2004; 2004US-0621004P.
PR 25-OCT-2004; 2004US-0621053P.
PR 25-OCT-2004; 2004US-0621072P.
PR 26-OCT-2004; 2004US-0621663P.
PR 27-OCT-2004; 2004US-0622016P.
PR 27-OCT-2004; 2004US-0622017P.
PR 27-OCT-2004; 2004US-0622320P.
PR 17-NOV-2004; 2004US-0628101P.
PR 17-NOV-2004; 2004US-0628112P.
PR 17-NOV-2004; 2004US-0628133P.
PR 17-NOV-2004; 2004US-0628134P.
PR 17-NOV-2004; 2004US-0628144P.
PR 17-NOV-2004; 2004US-0628145P.
PR 17-NOV-2004; 2004US-0628156P.
PR 17-NOV-2004; 2004US-0628165P.
PR 17-NOV-2004; 2004US-0628179P.
PR 17-NOV-2004; 2004US-0628190P.
PR 17-NOV-2004; 2004US-0628231P.
PR 17-NOV-2004; 2004US-0628251P.
PR 26-NOV-2004; 2004US-0630559P.
PR 08-DEC-2004; 2004US-0634075P.
PR 27-JAN-2005; 2005US-00043806.
XX (COMP-) COMPUGEN LTD.
PA (COHE/) COHEN Y.
PI Toporik A, Pollock S, Levine Z, Avalon-Soffer M, Cojocararu GS;
PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX WPI; 2005-810779/82.
XX New polynucleotide, useful for diagnosing a CRP variant-detectable disease or for selecting therapy for a CRP variant-detectable disease, e.g., myocardial infarction, coronary artery disease.
XX Disclosure; SEQ ID NO 439; 1670pp; English.
XX The invention relates to a new isolated polynucleotide. The polynucleotide is useful for diagnosing a CRP variant-detectable disease, for monitoring disease progression or treatment efficacy or relapse of a CRP variant-detectable disease or for selecting therapy for a CRP variant-detectable disease, e.g., myocardial infarction, coronary artery disease, non-fatal or fatal stroke, peripheral vascular disease, congestive heart failure or sudden cardiac death. The present sequence represents a human C-reactive protein, pentraxin-related (CRP) associated marker DNA.
XX SQ Sequence 3518 BP; 766 A; 1056 C; 907 G; 789 T; 0 U; 0 Other;
Query Match 84.3%; Score 1905; DB 14; Length 3518;
Best Local Similarity 94.8%; Pred. No. 1.7e-258;
Matches 2026; Conservative 0; Mismatches 0; Indels 111; Gaps 1;
QY 1 GAAATCAGGCTCCGGGCGGGCGGCGAAGGGGCGCAACTTCCCTCCCTCGGCGCCACCGGCT 60
DB 1489 GAAATCAGGCTCCGGGCGGGCGGCGAAGGGGCGCAACTTCCCTCCCTCGGCGCCACCGGCT 1548

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QY 61 CCGGGCGCTCCCTCGCGCCGAGCTTCAGCCGACGAGCTCCTGGGAGCGCGTCA 120
Db 1549 CCGCGCGCCCTCCCTCGCGCCGAGCTTCAGCCGACGAGCTCCTGGGAGCGCGTCA 1608
QY 121 TGGCCTTACCAAGTACCCGCTTGTCTCCGCTGCGCTTGTCTCCCAAGCCGCGCAGGC 180
Db 1609 TGGCCTTACCAAGTACCCGCTTGTCTCCGCTGCGCTTGTCTCCCAAGCCGCGCAGGC 1668
QY 181 CGAGCCAGTCCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAGC 240
Db 1669 CGAGCCAGTCCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAGC 1728
QY 241 TGAAGTCCAGGTGCTGTCTCCAAACCGACGTCGGGCTGTCTGGGCTCTCCAGCCGC 300
Db 1729 TGAAGTCCAGGTGCTGTCTCCAAACCGACGTCGGGCTGTCTGGGCTCTCCAGCCGC 1788
QY 301 CGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAACGAGCCCAAGGCGG 360
Db 1789 CGCGCGCGCGCGCAGTCCCACTTCTCTCTATACCTCTCCCAAAACGAGCCCAAGGCGG 1848
QY 361 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTCA 420
Db 1849 CCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCCTCA 1908
QY 421 CCCTGAGCGACTTCGCGCGAGAGAACGAGGGTACTATTCTGCTCGGCCCTGAGCAACT 480
Db 1909 CCCTGAGCGACTTCGCGCGAGAGAACGAGGGTACTATTCTGCTCGGCCCTGAGCAACT 1968
QY 481 CCATCATGTACTTTCAGCCACTTGTGCGGCTTCTCTCCAGCGAAGCCCAACGAGCGC 540
Db 1969 CCATCATGTACTTTCAGCCACTTGTGCGGCTTCTCTCCAGCGAAGCCCAACGAGCGC 2028
QY 541 CAGCGCCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCCCTGTCCTCGGCC 600
Db 2029 CAGCGCCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCCCTGTCCTCGGCC 2088
QY 601 CAGAGCGTGCGGGCACGCGGGGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGGCT 660
Db 2089 CAGAGCGTGCGGGCACGCGGGGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGGCT 2121
QY 661 GTGATATCTACATCTGGGCGCCCTTGGCGGCGACTTGTGGGTCTCTCTCTGTCACCTGG 720
Db 2122 ----- 2121
QY 721 TTATCACCCCTTTACTGCAACCAAGAAACGGAACGCTGTTTGCAAAATGTCCCGGCCTG 780
Db 2122 -----GGAACCGAAGACGTTTGTGCAAAATGTCCCGGCCTG 2157
QY 781 TGGTCAAAATCGGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 840
Db 2158 TGGTCAAAATCGGGAGACAAAGCCAGCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG 2217
QY 841 CCATACATTAATCTCAAACTGAGATCTCTCTTTTGGGAGCAAGTCTCTCCCTTTTCAT 900
Db 2218 CCATACATTAATCTCAAACTGAGATCTCTCTTTTGGGAGCAAGTCTCTCCCTTTTCAT 2277
QY 901 TTTTTCAGTCTTCTCCCTGTGTATTCATCTCATGATTAATTTTGTAGTGGGGCGGG 960
Db 2278 TTTTTCAGTCTTCTCCCTGTGTATTCATCTCATGATTAATTTTGTAGTGGGGCGGG 2337
QY 961 GTGGAAAGATTAATTTTCTTATGTGTGTGACCGGAAACAAAACTAGGTAAATCTTAC 1020
Db 2338 GTGGAAAGATTAATTTTCTTATGTGTGTGACCGGAAACAAAACTAGGTAAATCTTAC 2397
QY 1021 AGTACACCAAGGGTCACAATCTGTTGTGGCACATCGCGTAGGCGTGGAAAGGG 1080
Db 2398 AGTACACCAAGGGTCACAATCTGTTGTGGCACATCGCGTAGGCGTGGAAAGGG 2457
QY 1081 CAGGCCAGAGCTACCCGAGAGTCTTCAGAAATCATGCTGAGAGAGCTGGAGGCACCCATG 1140
Db 2458 CAGGCCAGAGCTACCCGAGAGTCTTCAGAAATCATGCTGAGAGAGCTGGAGGCACCCATG 2517
QY 1141 CCATCTCAACCTTCTCCCGCCGCTTTTACAAAGGGGGAGGCTTAAAGCCGAGAGAGCT 1200
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RESULT 13
AED96284
ID AED96284 standard; DNA; 3476 BP.
XX
AC AED96284;

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Db 2518 CCATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGGAGGCTTAAGCCGAGAGACAGCT 2577
QY 1201 TGATCAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCA 1260
Db 2578 TGATCAAAGGCACACAGCAAGTCAAGGTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCA 2637
QY 1261 GCTCAGGGCTCTTTCCTCCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG 1320
Db 2638 GCTCAGGGCTCTTTCCTCCACACCATTCAGGTCTTCTTCCGAGGCCCTGTCTCAGGG 2697
QY 1321 TGAGGTCTTGAGTCTCCACGCAAGGGAACAAGTACTTCTTGATACCTGGGATACGT 1380
Db 2698 TGAGGTCTTGAGTCTCCACGCAAGGGAACAAGTACTTCTTGATACCTGGGATACGT 2757
QY 1381 GCCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Db 2758 GCCCAGAGCCTCGAGGAGTAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 2817
QY 1441 AATGTAAACAATATCAGACTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 1500
Db 2818 AATGTAAACAATATCAGACTTTTATTAATCAAGCCTAAATTTGTATAGACCTAA 2877
QY 1501 AATAAATGAAGTGTGAGCTTAAACCTGGAAAATGAATCCTCTATCTCTAAAGAAAAT 1560
Db 2878 AATAAATGAAGTGTGAGCTTAAACCTGGAAAATGAATCCTCTATCTCTAAAGAAAAT 2937
QY 1561 CTCTGTGAAACCCCTATGTGGAGCGGAATGTCTCCAGCCCTTGCAITTCGAGAGGG 1620
Db 2938 CTCTGTGAAACCCCTATGTGGAGCGGAATGTCTCTCCAGCCCTTGCAITTCGAGAGGG 2997
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTAACAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 2998 CCCATGAAGAGGACAGGCTACCCCTTTAACAATAGAAATTTGAGCATCAGTGAGGTTAAA 3057
QY 1681 CTAAGGCCCTCTGAAATCTCTGAATTTGAGATACAAACATGTCTCTGGATCAGTGATGA 1740
Db 3058 CTAAGGCCCTCTGAAATCTCTGAATTTGAGATACAAACATGTCTCTGGATCAGTGATGA 3117
QY 1741 CTTTTTATCTTTGTAAGACAATTTGTTGGAGAGCCCTCTCACAGCCCTGCGCTCTGCT 1800
Db 3118 CTTTTTATCTTTGTAAGACAATTTGTTGGAGAGCCCTCTCACAGCCCTGCGCTCTGCT 3177
QY 1801 CAACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Db 3178 CAACTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 3237
QY 1861 CTGCTGTCCCAACACATGCACCTTCTGCTTAAGGTATGTTACAGCAATGCTGCCCCAT 1920
Db 3238 CTGCTGTCCCAACACATGCACCTTCTGCTTAAGGTATGTTACAGCAATGCTGCCCCAT 3297
QY 1921 GGAGAGAAAAAATTAAGTAGATAAGAAAATAAGAACCACTCATAAATCTTTCACCTTAGG 1980
Db 3298 GGAGAGAAAAAATTAAGTAGATAAGAAAATAAGAACCACTCATAAATCTTTCACCTTAGG 3357
QY 1981 AATAATCTCTGTTAAATAGGTGTACATCTCTCTGATTAATTTCTACACATAGTAA 2040
Db 3358 AATAATCTCTGTTAAATAGGTGTACATCTCTCTGATTAATTTCTACACATAGTAA 3417
QY 2041 AATATGCTTCTTTTAAATAGGTTGTTACTATGCTGTTATGATGCTGCTTTAATGAAT 2100
Db 3418 AATATGCTTCTTTTAAATAGGTTGTTACTATGCTGTTATGATGCTGCTTTAATGAAT 3477
QY 2101 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCA 2137
Db 3478 AAACATTTGTAGCATCTCTTTTAAATGGGTAAACAGCA 3514
```


| Query Match | 80.5% | Score 1821 | DB 14 | Length 3476 |
|---|--------------|------------------|------------|-------------|
| Best Local Similarity | 92.8% | Pred. No. 1e-246 | | |
| Matches 1984 | Conservative | 0 | Mismatches | 0 |
| | | | Indels | 153 |
| | | | Gaps | 1 |
| 26-JAN-2006 (first entry) | | | | |
| Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 441. | | | | |
| Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic; | | | | |
| Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial; | | | | |
| Immunosuppressant; cardiovascular-gen.; myocardial infarction; | | | | |
| cardiovascular disease; coronary artery disease; | | | | |
| cerebrovascular ischemia; peripheral vascular disease; | | | | |
| congestive heart failure; sudden cardiac death; | | | | |
| C-reactive protein pentraxin-related; CRP; genetic marker; ds. | | | | |
| Homo sapiens. | | | | |
| WO2005107364-A2. | | | | |
| 17-NOV-2005. | | | | |
| 27-JAN-2005; 2005WO-IB002407. | | | | |
| 27-JAN-2004; 2004US-0539128P. | | | | |
| 27-JAN-2004; 2004US-0539129P. | | | | |
| 22-OCT-2004; 2004US-0620874P. | | | | |
| 22-OCT-2004; 2004US-0621004P. | | | | |
| 25-OCT-2004; 2004US-0621053P. | | | | |
| 25-OCT-2004; 2004US-0621072P. | | | | |
| 26-OCT-2004; 2004US-0621663P. | | | | |
| 27-OCT-2004; 2004US-0622016P. | | | | |
| 27-OCT-2004; 2004US-0622017P. | | | | |
| 27-OCT-2004; 2004US-0622320P. | | | | |
| 17-NOV-2004; 2004US-0628101P. | | | | |
| 17-NOV-2004; 2004US-0628112P. | | | | |
| 17-NOV-2004; 2004US-0628133P. | | | | |
| 17-NOV-2004; 2004US-0628134P. | | | | |
| 17-NOV-2004; 2004US-0628144P. | | | | |
| 17-NOV-2004; 2004US-0628145P. | | | | |
| 17-NOV-2004; 2004US-0628156P. | | | | |
| 17-NOV-2004; 2004US-0628165P. | | | | |
| 17-NOV-2004; 2004US-0628179P. | | | | |
| 17-NOV-2004; 2004US-0628190P. | | | | |
| 17-NOV-2004; 2004US-0628231P. | | | | |
| 17-NOV-2004; 2004US-0628251P. | | | | |
| 26-NOV-2004; 2004US-0630559P. | | | | |
| 08-DEC-2004; 2004US-0634075P. | | | | |
| 27-JAN-2005; 2005US-00043806. | | | | |
| (COMP-) COMPUEN LTD. | | | | |
| (COHE/) COHEN Y. | | | | |
| Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocararu GS; | | | | |
| Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R; | | | | |
| WPI; 2005-810779/82. | | | | |
| New polynucleotide, useful for diagnosing a CRP variant-detectable | | | | |
| disease or for selecting therapy for a CRP variant-detectable | | | | |
| e.g., myocardial infarction, coronary artery disease. | | | | |
| Disclosure; SEQ ID NO 441; 1670pp; English. | | | | |
| The invention relates to a new isolated polynucleotide. The | | | | |
| polynucleotide is useful for diagnosing a CRP variant-detectable disease, | | | | |
| for monitoring disease progression or treatment efficacy or relapse of a | | | | |
| CRP variant-detectable disease or for selecting therapy for a CRP variant | | | | |
| -detectable disease, e.g., myocardial infarction, coronary artery | | | | |
| disease, non-fatal or fatal stroke, peripheral vascular disease, | | | | |
| congestive heart failure or sudden cardiac death. The present sequence | | | | |
| represents a human C-reactive protein, pentraxin-related (CRP) associated | | | | |
| marker DNA. | | | | |
| Sequence 3476 BP; 760 A; 1026 C; 886 G; 804 T; 0 U; 0 Other; | | | | |

Db 2356 AGTACACCAAGGGTACAAATCTGTTGTCGCACATCTCGCGTAGGCGTGGAAAGGG 2415
Qy 1081 CAGGCCAGAGCTACCCGACAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGCCACCCATG 1140
Db 2416 CAGGCCAGAGCTACCCGACAGAGTTCTCAGAAATCATGCTGAGAGAGCTGGAGCCACCCATG 2475
Qy 1141 CCATCTCAACCTCTTCCCGCCCGTTTTCACAAAGGGGAGGCTAAAGCCACAGACAGCT 1200
Db 2476 CCATCTCAACCTCTTCCCGCCCGTTTTCACAAAGGGGAGGCTAAAGCCACAGACAGCT 2535
Qy 1201 TGATCAAGGCACACAGAGCTAGGCTGAGAGAGCTGAGAGGACCTTGTCTCCCA 1260
Db 2536 TGATCAAGGCACACAGAGCTAGGCTGAGAGAGCTGAGAGGACCTTGTCTCCCA 2595
Qy 1261 GCTCAGGCTCTTTCCTCCACACATTCAGAGTCTTTCCTCCGAGGCCCTTGTCTCAGGG 1320
Db 2596 GCTCAGGCTCTTTCCTCCACACATTCAGAGTCTTTCCTCCGAGGCCCTTGTCTCAGGG 2655
Qy 1321 TGAGGTGCTTGAGTCTCCACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 1380
Db 2656 TGAGGTGCTTGAGTCTCCACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 2715
Qy 1381 GCCCAGAGCTCGAGAGGTAATGAAATTAAGAGAGAGACTGCCCTTTCGAGAGTCTAT 1440
Db 2716 GCCCAGAGCTCGAGAGGTAATGAAATTAAGAGAGAGACTGCCCTTTCGAGAGTCTAT 2775
Qy 1441 AATGTAACAATATCAGACTTTTTTTTTTATATCAAGCCTAAATTTGATAGACTTAA 1500
Db 2776 AATGTAACAATATCAGACTTTTTTTTTTATATCAAGCCTAAATTTGATAGACTTAA 2835
Qy 1501 AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 2836 AATAAAATGAAGTGTGAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAAGAAAT 2895
Qy 1561 CTCTGTGAACCCCTATGTGAGGCGGAATTTGCTCTCCAGGCCCTTGCAATTCAGAGGG 1620
Db 2896 CTCTGTGAACCCCTATGTGAGGCGGAATTTGCTCTCCAGGCCCTTGCAATTCAGAGGG 2955
Qy 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA 1680
Db 2956 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAGGTAAA 3015
Qy 1681 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 1740
Db 3016 CTAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCTGGGATCACTGATGA 3075
Qy 1741 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACAGCCCTGGCCCTCTGCT 1800
Db 3076 CTTTTTATCTTTGTAAGACAAATTTGAGAGGCCCTTCACAGCCCTGGCCCTCTGCT 3135
Qy 1801 CAACCTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
Db 3136 CAACCTAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 3195
Qy 1861 CTGCTGTCCCAACATGCACTCTCTTGTCTTAAGGTATGTTCAAGCAATGCTGCCCAT 1920
Db 3196 CTGCTGTCCCAACATGCACTCTCTTGTCTTAAGGTATGTTCAAGCAATGCTGCCCAT 3255
Qy 1921 GGAGAGAAAAAATTAAGTAGATAGGAAATGAAGAACCACTCATATTTCTTCACCTTAGG 1980
Db 3256 GGAGAGAAAAAATTAAGTAGATAGGAAATGAAGAACCACTCATATTTCTTCACCTTAGG 3315
Qy 1981 AATAATCTCTTAAATAGGTTGATCTTCTCGATTATTTCTACACATACATGATA 2040
Db 3316 AATAATCTCTTAAATAGGTTGATCTTCTCGATTATTTCTACACATACATGATA 3375
Qy 2041 AATATGCTCTTTTTTAAATAGGTTGATCTCTGCTGTTATGAGTGCTTTAATGAAT 2100
Db 3376 AATATGCTCTTTTTTAAATAGGTTGATCTCTGCTGTTATGAGTGCTTTAATGAAT 3435
Qy 2101 AAACATTTGTAGCATCTCTTAAATGGGTAAACAGCA 2137
|||||

Db 3436 AAACATTTGTAGCATCTCTTAAATGGGTAAACAGCA 3472

RESULT 14

AED96285 AED96285 standard; DNA; 3407 BP.

XX AED96285;

AC AED96285;

DT 26-JAN-2006 (first entry)

XX Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 442.

XX Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
KW Antirheumatic; Antinflammatory; Anticoagulant; Antimicrobial;
KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
KW cardiovascular disease; coronary artery disease;
KW cerebrovascular ischemia; peripheral vascular disease;
KW congestive heart failure; sudden cardiac death;
KW C-reactive protein pentraxin-related; CRP; genetic marker; ds.

XX Homo sapiens.

XX WO2005107364-A2.

XX 17-NOV-2005.

XX 27-JAN-2005; 2005WO-IB002407.

XX 27-JAN-2004; 2004US-0539128P.

XX 27-JAN-2004; 2004US-0539129P.

XX 22-OCT-2004; 2004US-0620874P.

XX 22-OCT-2004; 2004US-0621004P.

XX 25-OCT-2004; 2004US-0621053P.

XX 25-OCT-2004; 2004US-0621072P.

XX 26-OCT-2004; 2004US-0621663P.

XX 27-OCT-2004; 2004US-0622016P.

XX 27-OCT-2004; 2004US-0622017P.

XX 27-OCT-2004; 2004US-0622320P.

XX 17-NOV-2004; 2004US-0628101P.

XX 17-NOV-2004; 2004US-0628112P.

XX 17-NOV-2004; 2004US-0628133P.

XX 17-NOV-2004; 2004US-0628134P.

XX 17-NOV-2004; 2004US-0628144P.

XX 17-NOV-2004; 2004US-0628156P.

XX 17-NOV-2004; 2004US-0628165P.

XX 17-NOV-2004; 2004US-0628179P.

XX 17-NOV-2004; 2004US-0628190P.

XX 17-NOV-2004; 2004US-0628231P.

XX 17-NOV-2004; 2004US-0628251P.

XX 26-NOV-2004; 2004US-0630559P.

XX 08-DEC-2004; 2004US-0634075P.

XX 27-JAN-2005; 2005US-00043806.

(COMP-) COMPUEN LTD.

(COHE/) COHEN Y.

PI Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocaru GS;

PI Diber A, Novik A, Dahan D, Akiva P, Sorek R, Shemesh R;

XX WPI; 2005-810779/82.

XX New polynucleotide, useful for diagnosing a CRP variant-detectable
PT disease or for selecting therapy for a CRP variant-detectable disease,
PT e.g., myocardial infarction, coronary artery disease.

XX Disclosure; SEQ ID NO 442; 1670pp; English.

XX The invention relates to a new isolated polynucleotide. The
CC polynucleotide is useful for diagnosing a CRP variant-detectable disease,
CC for monitoring disease progression or treatment efficacy or relapse of a
CC CRP variant-detectable disease or for selecting therapy for a CRP variant

CC -detectable disease, e.g., myocardial infarction, coronary artery
CC disease, non-fatal or fatal stroke, peripheral vascular disease,
CC congestive heart failure or sudden cardiac death. The present sequence
CC represents a human C-reactive protein, pentraxin-related (CRP) associated
XX marker DNA.

SQ Sequence 3407 BP; 748 A; 1005 C; 871 G; 783 T; 0 U; 0 Other;

Query Match 74.4%; Score 1683; DB 14; Length 3407;
Best Local Similarity 89.6%; Pred. No. 2.4e-227;
Matches 1915; Conservative 0; Mismatches 0; Indels 222; Gaps 1;

QY 1 GAAATCAGGCTCGGCGCGCGCGAAGGGGCGCAACTTCCCTCGGCGCCCGCCGCT 60
DB 1489 GAAATCAGGCTCGGCGCGCGCGAAGGGGCGCAACTTCCCTCGGCGCCCGCCGCT 1548

QY 61 CCGCGCGCTCCCTCGGCGCGCGAGCTTCGAGCCAGCAGCGTCTCGGGAGCGGTCA 120
DB 1549 CCGCGCGCTCCCTCGGCGCGCGAGCTTCGAGCCAGCAGCGTCTCGGGAGCGGTCA 1608

QY 121 TGGCCCTTACAGTGACCGGCTTGCTCTCGCGCTGGCTTGCTGCCACGCGCCAGGC 180
DB 1609 TGGCCCTTACAGTGACCGGCTTGCTCTCGCGCTGGCTTGCTGCCACGCGCCAGGC 1668

QY 181 CGAGCAGTTCGGGTGTCGCGCTGGATCGAACCTGGAGCAGAGTGAGC 240
DB 1669 CGAGCAGTTCGGGTGTCGCGCTGGATCGAACCTGGAGCAGAGTGAGC 1728

QY 241 TGAAGTGCCAGGTGCTGCTCCACCCGACGCTCGGCTGCTGCTCTCCAGCGC 300
DB 1729 TGAAGTGCCAGGTGCTGCTCCACCCGACGCTCGGCTGCTGCTCTCCAGCGC 1788

QY 301 GCGGCGCGCGCCAGTCCACCTTCTCTATACCTTCCCAAAACAGCCCAAGCGC 360
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DB 2011 ----- 2010

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ID AED96281 standard; DNA; 3743 BP.
XX AED96281;
XX
XX 26-JAN-2006 (first entry)
XX Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 438.
DE
XX Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
XX Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
XX Immunosuppressant; cardiovascular-gen.; myocardial infarction;
XX cardiovascular disease; coronary artery disease;
XX cerebrovascular ischemia; peripheral vascular disease;
XX congestive heart failure; sudden cardiac death;
XX C-reactive protein pentraxin-related; CRP; genetic marker; ds.
XX
XX Homo sapiens.
XX
XX WO2005107364-A2.
XX 17-NOV-2005.
XX
XX 27-JAN-2005; 2005WO-IB002407.
XX
XX 27-JAN-2004; 2004US-0539128P.
XX 27-JAN-2004; 2004US-0539129P.
XX 22-OCT-2004; 2004US-0620874P.
XX 22-OCT-2004; 2004US-0621004P.
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XX 17-NOV-2004; 2004US-0628251P.
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XX 08-DEC-2004; 2004US-0634075P.
XX 27-JAN-2005; 2005US-00043806.
XX
XX (COMP-) COMPUGEN LTD.
XX (COHE/) COHEN Y.
XX
XX Toporik A, Pollock S, Levine Z, Ayalon-Soffer M, Cojocaru GS;
XX Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX WPI; 2005-810779/82.
XX
XX New polynucleotide, useful for diagnosing a CRP variant-detectable
XX disease or for selecting therapy for a CRP variant-detectable disease,

PT e.g., myocardial infarction, coronary artery disease.
XX
XX Disclosure; SEQ ID NO 438; 1670pp; English.
XX
XX The invention relates to a new isolated polynucleotide. The
XX polynucleotide is useful for diagnosing a CRP variant-detectable disease,
XX for monitoring disease progression or treatment efficacy or relapse of a
XX CRP variant-detectable disease or for selecting therapy for a CRP variant
XX -detectable disease, e.g., myocardial infarction, coronary artery
XX disease, non-fatal or fatal stroke, peripheral vascular disease,
XX congestive heart failure or sudden cardiac death. The present sequence
XX represents a human C-reactive protein, pentraxin-related (CRP) associated
XX marker DNA.
XX
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Best Local Similarity 89.6%; Pred. No. 2.4e-227;
Matches 1915; Conservative 0; Mismatches 0; Indels 222; Gaps 1;
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Qy 61 CCGGCGCGCTCCCTCGGCGCGCGCTTCAGCCACGAGCGTCTCGGAGCGCGTCA 120
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Qy 121 TGGCTTTACCAAGTACCGGCTTGTCTCTCGCGCTGGCTTGTCTCCACGCGCGCAGGC 180
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2127 | 94.1 | 2150 | 5 | US-10-131-831-9109 Sequence 9109, Ap |
| 2 | 1048 | 46.4 | 1060 | 2 | US-07-940-605A-11 Sequence 11, Appl |
| 3 | 1048 | 46.4 | 1060 | 2 | US-08-690-096-11 Sequence 11, Appl |
| 4 | 1048 | 46.4 | 1060 | 3 | US-09-023-655-1014 Sequence 1014, Ap |
| 5 | 346.8 | 24.0 | 1131 | 3 | US-08-751-512-7 Sequence 7, Appl |
| 6 | 193.8 | 8.6 | 803 | 2 | US-08-403-853-11 Sequence 11, Appl |
| 7 | 193.8 | 8.6 | 803 | 2 | US-09-477-737-2 Sequence 2, Appl |
| 8 | 193.8 | 8.6 | 972 | 2 | US-07-940-605A-9 Sequence 9, Appl |
| 9 | 193.8 | 8.6 | 972 | 2 | US-08-690-096-9 Sequence 9, Appl |
| 10 | 133.8 | 5.9 | 240 | 2 | US-08-628-417-6 Sequence 6, Appl |
| 11 | 131.6 | 5.8 | 1459 | 3 | US-09-537-654-3 Sequence 3, Appl |
| 12 | 131.6 | 5.8 | 1459 | 5 | US-10-818-809-3 Sequence 3, Appl |
| 13 | 131.4 | 5.8 | 1798 | 3 | US-09-797-906-1 Sequence 1, Appl |
| 14 | 131 | 5.8 | 2394 | 3 | US-09-800-729-33 Sequence 33, Appl |
| 15 | 130.6 | 5.8 | 1596 | 3 | US-09-835-811-1 Sequence 1, Appl |
| 16 | 130.6 | 5.8 | 2262 | 3 | US-09-311-021-171 Sequence 171, App |
| c 17 | 130.4 | 5.8 | 396 | 3 | US-09-640-173-53 Sequence 53, Appl |
| c 18 | 130.4 | 5.8 | 396 | 3 | US-09-713-550-53 Sequence 53, Appl |
| c 19 | 130.4 | 5.8 | 396 | 3 | US-09-825-294-53 Sequence 53, Appl |
| c 20 | 130.4 | 5.8 | 396 | 3 | US-09-970-966-53 Sequence 53, Appl |
| 21 | 130.4 | 5.8 | 2146 | 3 | US-10-003-392-3 Sequence 3, Appl |
| 22 | 130.4 | 5.8 | 2447 | 3 | US-09-014-969-14 Sequence 14, Appl |
| 23 | 129.6 | 5.7 | 3275 | 3 | US-09-370-838-151 Sequence 151, App |

ALIGNMENTS

RESULT 1
US-10-131-831-9109
; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Query Match 94.1%; Score 2127; DB 5; Length 2150;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2141; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Db 1 GGGTCATGGCCTTACCACTGACCGGCTTGGCTCGCTCGGCTGGCTTGGCTCGCTCGGCTG 60
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Db 61 CCAGGCCGAGCCAGTTCCGGGTGTCCGGCTGGATCGAACCTGGGCGGAGACAG 120
QY 235 TGGAGCTGAAGTCCAGGTGCTGTGTCCAAACCCAGTCGGGCTGCTCGTGGCTTTCC 294
Db 121 TGGAGCTGAAGTCCAGGTGCTGTGTCCAAACCCAGTCGGGCTGCTCGTGGCTTTCC 180
QY 295 AGCCGGGGGGCGCCCGGCGAGTCCACCTTCTTATCTTCTCCGAAACCAAGCCCA 354
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QY 355 AGCGGCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTGC 414
DB 241 AGCGGCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGGACACCTTGC 300
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DB 841 GCGGGGTGGGAAGATTACTTTTCTTTATGTGTTTTCACGGGAACAAACTAGGTAAA 900
QY 1015 ATCTACAGTACACACAGAGGTCACAATCTGTTGTGCGCACATCGCGGTAGGGCTGGA 1074
DB 901 ATCTACAGTACACACAGAGGTCACAATCTGTTGTGCGCACATCGCGGTAGGGCTGGA 960
QY 1075 AAGGGGAGGCGAGAGCTACCGCAGATTTCTCAGAACTCATGCTGAGAGGCTGGAGGCA 1134
DB 961 AAGGGGAGGCGAGAGCTACCGCAGATTTCTCAGAACTCATGCTGAGAGGCTGGAGGCA 1020
QY 1135 CCCATGCCATCTCAACCTTTCCCGCCGCTTTTACAAAGGGGGAGGCTAAAGCCCGAG 1194
DB 1021 CCCATGCCATCTCAACCTTTCCCGCCGCTTTTACAAAGGGGGAGGCTAAAGCCCGAG 1080
QY 1195 ACAGCTTGATCAAGGCGACACAGCAAGTCAGGGTTGGAGCAGTAGCTGAGGGGACTTGT 1254
DB 1081 ACAGCTTGATCAAGGCGACACAGCAAGTCAGGGTTGGAGCAGTAGCTGAGGGGACTTGT 1140
QY 1255 CTCCAGCTCAGGGCTCTTCTCCACACCAATTCAGGCTTCTTCTTTCGAGGCCCTGTG 1314
DB 1141 CTCCAGCTCAGGGCTCTTCTCCACACCAATTCAGGCTTCTTCTTTCGAGGCCCTGTG 1200
QY 1315 TCAGGGTCAGGTCTTGTAGTCTCCAAACGCGAGGGAACAAGTACTTCTTGATACCTGGGA 1374
DB 1201 TCAGGGTCAGGTCTTGTAGTCTCCAAACGCGAGGGAACAAGTACTTCTTGATACCTGGGA 1260
QY 1375 TACTGTGCCAGAGCCTCGAGGAGTAAATTAAGAAGAGAACTGCCTTTTGGCAGAG 1434
DB 1261 TACTGTGCCAGAGCCTCGAGGAGTAAATTAAGAAGAGAACTGCCTTTTGGCAGAG 1320
QY 1435 TTCTATAATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCTAAAAATGTATAG 1494

DB 1321 TTCTATAATGTAAACAATATCAGAC-TTTTTTTTTTATAATCAAGCCTAAAAATGTATAG 1379
QY 1495 ACCTAAATAAATAAGAGTGGTGAAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAA 1554
DB 1380 ACCTAAATAAATAAGAGTGGTGAAGCTTAACCCCTGGAAATGAATCCCTCTATCTCTAAA 1439
QY 1555 GAAATCTCTGTGAAACCCCTATGTGAGGGGGAATTCCTCTCCAGGCCCTTGATGCA 1614
DB 1440 GAAATCTCTGTGAAACCCCTATGTGAGGGGGAATTCCTCTCCAGGCCCTTGATGCA 1499
QY 1615 GAGGGGCCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAG 1674
DB 1500 GAGGGGCCATGAAAGAGGACAGGCTACCCCTTTACAAATAGAATTTGAGCATCAGTGAG 1559
QY 1675 GTTAAACTAAGAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCAC 1734
DB 1560 GTTAAACTAAGAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCAC 1619
QY 1735 TGATGACTTTTATATCTTTGTAAAGCAAATTTGTTGGAGAGCCCTCAACAGCCCTTGCC 1794
DB 1620 TGATGACTTTTATATCTTTGTAAAGCAAATTTGTTGGAGAGCCCTCAACAGCCCTTGCC 1679
QY 1795 TCTGCTCAACTAGCAGATACAGGGATGAGGCGAGACCTGACTCTCTTAAGGAGGCTGAGAG 1854
DB 1680 TCTGCTCAACTAGCAGATACAGGGATGAGGCGAGACCTGACTCTCTTAAGGAGGCTGAGAG 1739
QY 1855 CCCAAACTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGTTCAAGCAATGCTG 1914
DB 1740 CCCAAACTGCTGTCCCAACATGCACTTCTTGTCTTAAGGTATGTTCAAGCAATGCTG 1799
QY 1915 CCCATTGGAGAGAAAAAATTAAAGTAAAGAAATTAAGAACCACTCATTAATTTCTTAC 1974
DB 1800 CCCATTGGAGAGAAAAAATTAAAGTAAAGAAATTAAGAACCACTCATTAATTTCTTAC 1859
QY 1975 CTTAGGAATATCTCCTGTTAAATATGTTGATACATTTCTCCTGATTTATTTCTACACATAC 2034
DB 1860 CTTAGGAATATCTCCTGTTAAATATGTTGATACATTTCTCCTGATTTATTTCTACACATAC 1919
QY 2035 ATGTAAATAATGCTCTTTCTTTTAAATAGGGTTGTACTATGCTGTTATGATGCTTTA 2094
DB 1920 ATGTAAATAATGCTCTTTCTTTTAAATAGGGTTGTACTATGCTGTTATGATGCTTTA 1979
QY 2095 ATGAATAAACATTTGTAGCATCTCTTTTAAATAGGGTAAACAGCAAAAAAATAAAAAA 2154
DB 1980 ATGAATAAACATTTGTAGCATCTCTTTTAAATAGGGTAAACAGCATCCGAAAAAATA 2039
QY 2155 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2214
DB 2040 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2099
QY 2215 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2261
DB 2100 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2146

RESULT 2

US-07-940-605A-11
; Sequence 11, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUPPO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711


```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-940-605A-11

Query Match 46.4%; Score 1048; DB 2; Length 1060;
Best Local Similarity 100.0%; Pred. No. 1.8e-217;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 CCGCTCCCTCGCGCCGAGCTTCGAGCCAAAGAGCGTCTCGGGAGCGCGTCATGGCT 126
DB 13 CGCTCCCTCGCGCCGAGCTTCGAGCCAAAGAGCGTCTCGGGAGCGCGTCATGGCT 72
QY 127 TACCACTGACCGCTTGCTCTCGCGCTGCTGCTCCAGCGCGCGCGAGCC 186
DB 73 TACCACTGACCGCTTGCTCTCGCGCTGCTGCTCCAGCGCGCGCGAGCC 132
QY 187 AGTTCGGGTGTCGCGCTGATCGGACCTGGAACCTGGCGGAGACAGTGGAGCTGAAGT 246
DB 133 AGTTCGGGTGTCGCGCTGATCGGACCTGGAACCTGGCGGAGACAGTGGAGCTGAAGT 192
QY 247 GCCAGGTGCTGTGTCACACCGAGCTCGGGTGTCTGCTGCTTCACGCGCGCGCG 306
DB 193 GCCAGGTGCTGTGTCACACCGAGCTCGGGTGTCTGCTGCTTCACGCGCGCGCG 252
QY 307 CGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAGAGCGCGCGCGCGAGG 366
DB 253 CGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAGAGCGCGCGCGCGAGG 312
QY 367 GCGTGGACACCCAGCGGTTCGCGCAAGAGGTTCGGGAGACACCTTCGTCCTCACCTGA 426
DB 313 GCGTGGACACCCAGCGGTTCGCGCAAGAGGTTCGGGAGACACCTTCGTCCTCACCTGA 372
QY 427 GCGACTTCGCGGAGAGAACAGGCTACTATTTCGTTCGCGCTGAGCAACTCCATCA 486
DB 373 GCGACTTCGCGGAGAGAACAGGCTACTATTTCGTTCGCGCTGAGCAACTCCATCA 432
QY 487 TGTAATTCAGCACTTCGTGCGGTCTTCCTGCGAGCGAGCGCCACGAGCGCGAGCG 546
DB 433 TGTAATTCAGCACTTCGTGCGGTCTTCCTGCGAGCGAGCGCCACGAGCGCGAGCG 492
QY 547 CGCGACCAACACACCGCGCGCCACCATCGCGTTCGCGAGCGCTTCCTGCGCGCGAGG 606
DB 493 CGCGACCAACACACCGCGCGCCACCATCGCGTTCGCGAGCGCTTCCTGCGCGCGAGG 552
QY 607 CGTCCGCGCACGCGCGCGCGCGAGTGACACACGAGGGGCTGGAGCTTCGCTGTGATA 666
DB 553 CGTCCGCGCACGCGCGCGCGCGAGTGACACACGAGGGGCTGGAGCTTCGCTGTGATA 612
QY 667 TCTACATCTGGCGCGCTTCGCGCGGAGCTTCGTGGGGTCTTCCTCTGTCACGTGGTATCA 726
DB 613 TCTACATCTGGCGCGCTTCGCGCGGAGCTTCGTGGGGTCTTCCTCTGTCACGTGGTATCA 672
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QY 727 CCCTTTACTGCAACACACAGAACCGAAGACGTGTTTGCAAAATGTCCCGCGCTGTGCTCA 786
DB 673 CCCTTTACTGCAACACACAGAACCGAAGACGTGTTTGCAAAATGTCCCGCGCTGTGCTCA 732
QY 787 AATCGGAGACAAGCCCGAGCCCTTCGCGGAGATACGTCTTAACCCCTGTGCAACAGCCACTA 846
DB 733 AATCGGAGACAAGCCCGAGCCCTTCGCGGAGATACGTCTTAACCCCTGTGCAACAGCCACTA 792
QY 847 CATTACTTCAAACTGAGATCCTCTTTTGAGGGAGCAAGTCTTCCCTTCATTTTTC 906
DB 793 CATTACTTCAAACTGAGATCCTCTTTTGAGGGAGCAAGTCTTCCCTTCATTTTTC 852
QY 907 CAGTCTTCCTCCTGCTGATTCATCTCATGATTAATTTTAGTGGGGCGGGGTGGGA 966
DB 853 CAGTCTTCCTCCTGCTGATTCATCTCATGATTAATTTTAGTGGGGCGGGGTGGGA 912
QY 967 AAGATTACTTTTCTTTATGTTTGACGGGAAAACAAACTAGGTAAATCTACAGTACA 1026
DB 913 AAGATTACTTTTCTTTATGTTTGACGGGAAAACAAACTAGGTAAATCTACAGTACA 972
QY 1027 CCACAAGGTCACAATACTGTTGTCGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC 1086
DB 973 CCACAAGGTCACAATACTGTTGTCGCACATCGCGGTAGGCGGTGGAAGGGCGAGGCC 1032
QY 1087 AGAGCTACCCGCGAGAGTTCTCAGAATCA 1114
DB 1033 AGAGCTACCCGCGAGAGTTCTCAGAATCA 1060

RESULT 3
US-08-690-096-11
; Sequence 11, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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| | | | |
|--------------------------------|------|---|------|
| ; MOLECULE TYPE: DNA (genomic) | | US-08-690-096-11 | |
| Query Match | | 46.4%; Score 1048; DB 2; Length 1060; | |
| Best Local Similarity | | 100.0%; Pred. No. 1.8e-217; | |
| Matches 1048; Conservative | | 0; Mismatches 0; Indels 0; Gaps 0; | |
| Qy | 67 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCATGGCCT | 126 |
| Db | 13 | CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCATGGCCT | 72 |
| Qy | 127 | TACAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCGACAGGCCGAGCC | 186 |
| Db | 73 | TACAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCGACAGGCCGAGCC | 132 |
| Qy | 187 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGCGAGACAGTGAGTGAAGT | 246 |
| Db | 133 | AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGCGAGACAGTGAGTGAAGT | 192 |
| Qy | 247 | GCCAGGTGCTGTCTCCACCGAGTCTGGCTGTCTGTGGCTCTTCCAGCGCGCGCGG | 306 |
| Db | 193 | GCCAGGTGCTGTCTCCACCGAGTCTGGCTGTCTGTGGCTCTTCCAGCGCGCGCGG | 252 |
| Qy | 307 | CCGCCGCGAGTCCACCTTCTCTATACCTCTCCAAACAAAGCCAAAGCGCCGAGG | 366 |
| Db | 253 | CCGCCGCGAGTCCACCTTCTCTATACCTCTCCAAACAAAGCGCCGAGCGCGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCTCAACCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCGTCTCAACCTGA | 372 |
| Qy | 427 | GCGACTTCGCGGAGAGAAAGAGGCTACTATTTCTGCTCGGCTGAGCAACTCCATCA | 486 |
| Db | 373 | GCGACTTCGCGGAGAGAAAGAGGCTACTATTTCTGCTCGGCTGAGCAACTCCATCA | 432 |
| Qy | 487 | TGTACTTCAGCCACTTCGTGCGGCTTCTTCGCGAGGAAAGCCACACGAGCGCAGCG | 546 |
| Db | 433 | TGTACTTCAGCCACTTCGTGCGGCTTCTTCGCGAGGAAAGCCACACGAGCGCAGCG | 492 |
| Qy | 547 | CGCGACCAACACCGCGCGCCACCATCGCGTCCGAGCGCCCTGTCTCGCGCCAGAGG | 606 |
| Db | 493 | CGCGACCAACACCGCGCGCCACCATCGCGTCCGAGCGCCCTGTCTCGCGCCAGAGG | 552 |
| Qy | 607 | CGTCCGCGCAGCGCGCGCGCGCGAGTGACACAGAGGGGCTGACTTCGCTGTGATA | 666 |
| Db | 553 | CGTCCGCGCAGCGCGCGCGCGCGAGTGACACAGAGGGGCTGACTTCGCTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTACTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTACTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGGCTGTGTGTA | 786 |
| Db | 673 | CCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAAATGTCCCGGCTGTGTGTA | 732 |
| Qy | 787 | AATCGGAGACAAGCCAGCCCTTTCGCGAGATAGTCTTAACCTCTGTGCAACAGCCACTA | 846 |
| Db | 733 | AATCGGAGACAAGCCAGCCCTTTCGCGAGATAGTCTTAACCTCTGTGCAACAGCCACTA | 792 |
| Qy | 847 | CATTACTTCAAACTGAGATCCTTCTCTTGGGAGCAAGTCTTCCCTTTTCATTTTTC | 906 |
| Db | 793 | CATTACTTCAAACTGAGATCCTTCTCTTGGGAGCAAGTCTTCCCTTTTCATTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCCTGTGTATTCATTTCTCATGATTAATTTTGTGGGGCGGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCCTGTGTATTCATTTCTCATGATTAATTTTGTGGGGCGGGGTGGGA | 912 |
| Qy | 967 | AAGATTACTTTTCTTTATGTTTGAAGGAAACAAACTAGGTAAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTACTTTTCTTTATGTTTGAAGGAAACAAACTAGGTAAATCTACAGTACA | 972 |
| Qy | 1027 | CCACAAGGTCACAATACTGTTGTGCGCACATCGCGGTAGGCGGTGGAAAGGGCGAGCC | 1086 |

US-09-023-655-1014
; Sequence 1014, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179145
US-09-023-655-1014

Query Match 46.4%; Score 1048; DB 3; Length 1060;
Best Local Similarity 100.0%; Pred. No. 1.8e-217;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 67 CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCATGGCCT 126
Db 13 CGCTCCCTCGCGCCGAGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTCATGGCCT 72
Qy 127 TACAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCGACAGGCCGAGCC 186
Db 73 TACAGTGACCGCTTGTCTCTCGCGTGGCTTGTCTCCACGCCGACAGGCCGAGCC 132
Qy 187 AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGCGAGACAGTGAGTGAAGT 246
Db 133 AGTTCCGGGTGTCCCGCTGGATCGGACCTGGAACTCTGGCGAGACAGTGAGTGAAGT 192
Qy 247 GCCAGGTGCTGTCTGTCCAAACCGCAGTCTCGGGTGTCTGTGGCTCTTCCAGCGCGCGCGG 306

Db 193 GCCAGGTGCTGTGTCACACCCGAGCTCGGGTGTCTGTGGCTTTCACGCGCGCGGG 252
Qy 307 CGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAACAAAGCCCAAGCGCGCGAGG 366
Db 253 CGCGCGCCAGTCCCACTTCTCTATACCTCTCCCAAAACAAAGCCCAAGCGCGAGG 312
Qy 367 GCGTGACACCCAGCGGGTCTCGGGCAAGAGGTGGGGACACCTTCGTCCTCACCTGA 426
Db 313 GCGTGACACCCAGCGGGTCTCGGGCAAGAGGTGGGGACACCTTCGTCCTCACCTGA 372
Qy 427 GCGACTTCGCGGAGAGAGGAGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCA 486
Db 373 GCGACTTCGCGGAGAGAGGAGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCA 432
Qy 487 TGTACTTCAGCCACTTCGTGCGGGTCTTCCTCGCAGCGAAGCCACACGAGCCAGCGC 546
Db 433 TGTACTTCAGCCACTTCGTGCGGGTCTTCCTCGCAGCGAAGCCACACGAGCCAGCGC 492
Qy 547 CGCGACCAACACACCGCGCCCAACATCGCTGCGAGCCCTGTCTCGCCCGCAGAGG 606
Db 493 CGCGACCAACACACCGCGCCCAACATCGCTGCGAGCCCTGTCTCGCCCGCAGAGG 552
Qy 607 CGTGCGCGCAGCGGGGGGCGAGTGCACAGAGGGGCTGCACTTCGCTGTGATA 666
Db 553 CGTGCGCGCAGCGGGGGGCGAGTGCACAGAGGGGCTGCACTTCGCTGTGATA 612
Qy 667 TCTACATCTGGCGGCTTGGCGGGACTTGTGGGTCTTCTCTGCTCACTGGTTATCA 726
Db 613 TCTACATCTGGCGGCTTGGCGGGACTTGTGGGTCTTCTCTGCTCACTGGTTATCA 672
Qy 727 CCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAATGTCCCGGCTGTGGTCA 786
Db 673 CCCTTTACTGCAACACAGGAACCGAAGACGTGTTTGCAAATGTCCCGGCTGTGGTCA 732
Qy 787 AATCGGAGACAAAGCCAGCCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCCACTA 846
Db 733 AATCGGAGACAAAGCCAGCCCTTTCGGCGAGATAGTCTAAACCTGTGCAACAGCCACTA 792
Qy 847 CATTACTTCAAACTGAGATCTCTCTTTTGGGAGCAAGTCTTCCCTTCATTTTTC 906
Db 793 CATTACTTCAAACTGAGATCTCTCTTTTGGGAGCAAGTCTTCCCTTCATTTTTC 852
Qy 907 CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTATGTTGGGGCGGGTGGGA 966
Db 853 CAGTCTTCTCCTGTGTATTCATTTCTCATGATTAATTTTATGTTGGGGCGGGTGGGA 912
Qy 967 AAGATTACTTTTCTTTATGTTTGAACGGGAAACAAACTAGGTAAATCTACAGTACA 1026
Db 913 AAGATTACTTTTCTTTATGTTTGAACGGGAAACAAACTAGGTAAATCTACAGTACA 972
Qy 1027 CCACAAGGTCAATATCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC 1086
Db 973 CCACAAGGTCAATATCTGTTGCGCACATCGCGGTAGGCGTGGAAAGGGCGAGGCC 1032
Qy 1087 AGAGCTACCCGAGAGTTCTCAGAAATCA 1114
Db 1033 AGAGCTACCCGAGAGTTCTCAGAAATCA 1060

RESULT 5

US-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramey, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified PAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Matthew B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1131 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1128
US-08-751-512-7

Query Match 24.0%; Score 543; DB 3; Length 1131;
Best Local Similarity 100.0%; Pred. No. 5.9e-108;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 ATGGCTTTACCAAGTACCGCCCTTGTCTGTGCGCTGGCTTGTCTGTCTCAACGCGCCAGG 179
Db 1 ATGGCTTTACCAAGTACCGCCCTTGTCTGTGCGCTGGCTTGTCTGTCTCAACGCGCCAGG 60
Qy 180 CCGAGCCAGTTCCGGGTGTCCGGCTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCCGGGTGTCCGGCTGGATCGGACTGGAACTGGGCGAGACAGTGGAG 120
Qy 240 CTGAAGTCCAGAGTCTGTCTGTCAACCGAGCTCGGCTGTCTGTGGCTCTTCCAGCCG 299
Db 121 CTGAAGTCCAGAGTCTGTCTGTCAACCGAGCTCGGCTGTCTGTGGCTCTTCCAGCCG 180
Qy 300 CGCGCGCGCGCGCGAGTCCCACTTCTCTCTATACCTTCTCCCAAAACAAAGCCCAAGGCG 359
Db 181 CGCGCGCGCGCGCGAGTCCCACTTCTCTCTATACCTTCTCCCAAAACAAAGCCCAAGGCG 240
Qy 360 GCGGAGGGGTGGACACCCAGCGGTTCCTGGGCAAGAGTTGGGGGACACCTTCGTCCTC 419
Db 241 GCGGAGGGGTGGACACCCAGCGGTTCCTGGGCAAGAGTTGGGGGACACCTTCGTCCTC 300
Qy 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTCGGCCCTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGTCTGGGCCCTGAGCAAC 360
Qy 480 TCCATCATGTATTTTCAAGCCACTTCGTGCGGGTTCCTCTGCCAGCGAAGCCCAACGAGC 539
Db 361 TCCATCATGTATTTTCAAGCCACTTCGTGCGGGTTCCTCTGCCAGCGAAGCCCAACGAGC 420
Qy 540 CCAGCGCGCGCGCGACCAACACCGCGGCCCAACCATCGGCTGCGAGCCCTGTCCCTGCGC 599
Db 421 CCAGCGCGCGCGCGACCAACACCGCGGCCCAACCATCGGCTGCGAGCCCTGTCCCTGCGC 480
Qy 600 CCAGAGGGGTGCGCGCGAGCGCGGGGGCGCGAGTGCACACAGAGGGGTGACTTCGCGC 659
Db 481 CCAGAGGGGTGCGCGCGAGCGCGGGGGCGCGAGTGCACACAGAGGGGTGACTTCGCGC 540
Qy 660 TGT 662
|||

QY 650 GGACTTCGCTGTGATATCTACATCTGGCGGCCCTTGGCGGAGCTGTGGGTCCTTCT 709
Db |||||
579 GGACTTCGCTGTGATATCTACATCTGGCGGCCCTTGGCGGAGCTGTGGGTCCTTCT 638
QY 710 CTGTCTACCTGTTATCACCTTTTACTGCAACACACAGGACCGAAGAGCTGTTTGCAGATG 769
Db |||||
639 GCTGTCTTGTATCATCTCTCATCTGCTTACACAGAGCCGGAAGCGGTGTTTGCAGATG 698
QY 770 TCCCGGCTGTGGTCAAAATCGGGAGACAAGCCAGCCCTTTCGGCGAGATAGCTCTAAAC 829
Db |||||
699 TCCAGGCGCTAGTCAGACAGGAGGCAAGCCAGACCTTCAGAGAAAATTGTGTAATA 758
QY 830 CTGTGCAACAGCCTACTATTAATCTCAAACTAGATC 866
Db |||||
759 TGGCACCGCCAGGAAGCTACAACCTACTATGACTTC 795

RESULT 8

US-07-940-605A-9
; Sequence 9, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-940-605A-9

Query Match 8.6%; Score 193.8; DB 2; Length 972;
Best Local Similarity 61.1%; Pred. No. 2.8e-32;
Matches 426; Conservative 0; Mismatches 247; Indels 24; Gaps 6;
QY 185 CCAGTTCGGGTGTCCGCTGGATCGGACCTGGACCTGGCGGAGACAGTGGAGTGA 244
Db |||||
222 CGAATCCGGAATCTTTCAGAGAAAATGGACCCGAACTTGGTCAGAGGTGGACCTGGT 281
QY 245 GTGCAGGTGCTGTGTCACACCCGACGCTCGGGCTCTCGTGGCTCTTCCAGCGCGGG 304
Db |||||
282 ATGTGAAGTGTGGGTGCGTTTGCAGAGGATGCTCTTGGCTCTTCCAGAACTCCAGTTC 341
QY 305 CGCGCCGCGCAGTCCCACTCTCTCTTACCT-----CTCCCAAAACAAGCCCAAGGC 358

Db |||||
342 CAAACTCCCGCCACCTTCGTTGTCTATATGGCTTCATCCCAACAAGATAACGTG 401
QY |||||
359 GCGCAGGCGCTGGA---CACCCAGGCTTCTGGGCAAGAG---TTGGGGACACCTT 412
Db |||||
402 GACGAGAGCTGAATTCGCGAAACTGTTTTCTGCCATGAGGAGACCAAAATAAAGTA 461
QY 413 CGTCTCACCTTCAGCGACTTCCGCGAGAGAACGAGGGCTACTATTCTGTCTCGGCCCT 472
Db |||||
462 CGTTCTCACCTTGAACAAGTTTCAAGCAAGGAAAAAGAGGCTACTATTCTGTCTAGTCAT 521
QY 473 GAGCAACTCCATCATGTACTTTCAGCCACTTCGTGCGGCTCTTCTGCCAGGAGCCAC 532
Db |||||
522 CAGCAACTCGGTGATGTTTCACTTCTGTCGTCAGTCTTTCAGAAAAGTGAACCTCTAC 581
QY 533 CAGGAC---GCCAGCGCGCAGCACCAACACCGCGGCCACCATCGCGTCCGAGCCCT 589
Db |||||
582 TACTACAGCCAGTGTGCGAACTTCTCCTCCTGTGCACTTCCCGGAC---ATCTCA 638
QY 590 GTCCCTGCGCCAGAGGCTGCGGCCAGCGCGGGGCGCAGTGCACACGAGGGGGCT 649
Db |||||
639 GCCCAGAGACCAAGATTGTCGGC-----CCCGTGGCTCAGTGAAGGGGACCGATT 692
QY 650 GGACTTCGCTGTGATATCTACATCTGGCGGCCCTTGGCGGAGACTTGTGGGTCCTTCT 709
Db |||||
693 GGACTTCGCTGTGATATTTACATCTGGGCACCTTGGCGGAAATCTGGCTGGCCCTTCT 752
QY 710 CCGTCACTGGTTATCACCTTTTACTGCAACACACAGGACCGAAGACGTTTGCAGATG 769
Db |||||
753 GCTGCTTGTATCATCATCTCATCTGTACACAGGAGCCGAAAGCGTGTGTGCAATG 812
QY 770 TCCCGGCTGTGTCAAATCGGAGACAAGCCAGCTTTCGGCGAGATAGCTCTAAC 829
Db |||||
813 TCCAGGCGCTAGTCAGACAGGAGGCAAGCCAGACCTTCAGAGAAAATTGTGTAATA 872
QY 830 CTGTGCAACAGCCTACTATTAATCTTCAAACTAGATC 866
Db |||||
873 TGGCACCGCCAGGAAGCTACAACCTACTATGACTTC 909

RESULT 9

US-08-690-096-9
; Sequence 9, Application US/08690096
; Patent No. 5945513
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184

```
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-690-096-9

Query Match      8.6%; Score 193.8; DB 2; Length 972;
Best Local Similarity 61.1%; Pred. No. 2.8e-32;
Matches 426; Conservative 0; Mismatches 247; Indels 24; Gaps 6;

Qy 185 CCAGTTCGGGTGTCGGCGCTGGATCGGACCTGGGCGAGACAGTGGAGCTGAA 244
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 222 CGAACTCCGAATCTTCCAAAGAAATGAGCGCCGAATCTGGTCAGAGGTGGACCTGGT 281
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 245 GTGCCAGGTGCTGTGCCAACCGACGTCGGGTGCTCGTGGCTCTTCCAGCGCGCGG 304
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 282 ATGTGAAGTGTGGGTCCGTTTCGCAAGGATGCTCTTGGCTCTTCCAGAACTCCAGCTC 341
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 CGCGCGCGCAGTCCCACTTCTCTATACCT-----CTCCAAACCAAGCCCAAGGC 358
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 342 CAAACTCCCCCAGCCACCTTCGTTGTCTATATGCTTCATCCCAACAAGATAACGTG 401
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 359 GGCCGAGGGCTGA---CACCCAGCGTTCTCGGCNAGAG---TTGGGGGACACCTT 412
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 402 GGACGAGAAGCTGAATTCGTGCAAACTGTTTCTGCCATGAGGACACGAATAAAGTA 461
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 413 CGTCTCACCCTGAGCGACTTCCCGGAGAGAAACGAGGGCTACTATTCTCTCGGCCCT 472
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 462 CGTCTCACCCTGAGCGACTTCCCGGAGAGAAACGAGGGCTACTATTCTCTCGTCTCAT 521
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 473 GAGCAACTCCATCATGATCTTACGCCACTTCGTGCGCGGTCTTCTGCGCAGCGAAGCCCAAC 532
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 522 CAGCAACTCGGTGATGATCTTCACTTCTGTCTGTCGCACTCTTCCAGAAAGTGAACCTCTAC 581
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 533 CACGAC---GCCAGCGCGCACACCAACACCGCGGCCACCATCGGTGCGAGCCCT 589
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 582 TACTACCAAGCCAGTGTGCGAACTCCCTCACCCTGTGCACCCCTACCGGGAC---ATCTCA 638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 590 GTCCCTCGCCGACAGCGGTGCGGCCAGCGCGCGGGGGCGCAGTGCAACAGCGGGGCT 649
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 639 GCGCCAGAGACAGAGATTGTCGGC-----CCGCTGGCTCAGTGAAGGGGACCGGATT 692
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 650 GGACTTCGCTGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCT 709
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 693 GGACTTCGCTGTGATATTACATCTGGGCGCCCTTGGCGGGAACTCTGCGTGGCCCTTCT 752
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 710 CTTGTACTGTTATCACCCTTTACTGCAACACAGGACCGAGACGTGTTTGCATATG 769
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 753 GCTGTCTTGTATCATCTCTCATCTGTCTACACAGGAGCGGAAAGCGTGTTCGCAATG 812
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 770 TCCCGCGCTGTGTGTAATCGGAGCAAGCCAGCGCTTTCGGCGAGATACGTCCTAAC 829
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 813 TCCAGCGCGGTAGTCAGACGAGGAGGCGGACCCAGACCTTCAGAGAAATTTGTGTA 872
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 830 CTGTGCAACGCCACTACATTTACTTCAACTGAGATC 866
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 873 TGGCAGCCGCGAGGAGCTACAACTACTACATGACTTC 909
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
us-08-628-417-6
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
```

```

; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESSEE: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BIFFONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match      5.9%; Score 133.8; DB 2; Length 240;
Best Local Similarity 87.0%; Pred. No. 1.5e-19;
Matches 147; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 2093 TAATGATTAACATTTCTAGCATCTCTTTAATGGTAAACAGCAAAAAAAAAAAAAA 2152
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2153 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2212
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 67 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 126
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2213 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 127 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 175
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-09-537-654-3
; Sequence 3, Application US/09537654
; Patent No. 6720478
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; APPLICANT: Shi, Jinrui
; TITLE OF INVENTION: A No. 6720478e1 Maize Rad51-Like Gene and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1107
; CURRENT APPLICATION NUMBER: US/09/537,654
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: 60/132,582
; EARLIER FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1459
; TYPE: DNA
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (169)...(1011)
US-09-537-654-3

Query Match 5.8%; Score 131.6; DB 3; Length 1459;
Best Local Similarity 93.8%; Pred. No. 1e-18;
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2116 CCTCTTTAATGGTTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2175
Db 1294 CTTCTCTGATCACCATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1353
Qy 2176 AA 2235
Db 1354 AA 1413
Qy 2236 AA 2261
Db 1414 AA 1439

RESULT 12
US-10-818-809-3
Sequence 3, Application US/10818809
Patent No. 7034117
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Shi, Jinrui
TITLE OF INVENTION: Rad51C Polypeptides and Uses Thereof
FILE REFERENCE: 1107D
CURRENT APPLICATION NUMBER: US/10/818,809
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: 60/132,582
PRIOR FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 1459
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (169)...(1011)
US-10-818-809-3

Query Match 5.8%; Score 131.6; DB 5; Length 1459;
Best Local Similarity 93.8%; Pred. No. 1e-18;
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2116 CCTCTTTAATGGTTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2175
Db 1294 CTTCTCTGATCACCATCAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1353
Qy 2176 AA 2235
Db 1354 AA 1413
Qy 2236 AA 2261
Db 1414 AA 1439

RESULT 13
US-09-797-906-1
Sequence 1, Application US/09797906
Patent No. 6329188
GENERAL INFORMATION:
APPLICANT: Zianghe Yan, Karen A. Ketchum, Valentina DiFrancesco, Ellen M. Beasley
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1798
TYPE: DNA
ORGANISM: Human
US-09-797-906-1

Query Match 5.8%; Score 131.4; DB 3; Length 1798;
Best Local Similarity 89.8%; Pred. No. 1.3e-18;
Matches 141; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Qy 2105 ATTTCTAGCATCTCTTTAATGGTTAAACAGCAAAAAAAAAAAAAAAAAAAAAA 2164
Db 1620 ATTACAAACATGCTCTTGGCAGTGGAAAAA 1679
Qy 2165 AA 2224
Db 1680 AA 1739
Qy 2225 AA 2261
Db 1740 AA 1776

RESULT 14
US-09-800-729-33
Sequence 33, Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 2394
TYPE: DNA
ORGANISM: Homo sapiens
US-09-800-729-33

Query Match 5.8%; Score 131; DB 3; Length 2394;
Best Local Similarity 96.4%; Pred. No. 1.8e-18;
Matches 134; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2123 AATGGTTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2182
Db 2249 AAAAGGAAAAAAGGAAAAA 2308
Qy 2183 AA 2242
Db 2309 AA 2368
Qy 2243 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db 2369 AAAAAAAAAAAAAAAAAAAAAA 2387

RESULT 15
US-09-835-811-1
Sequence 1, Application US/09835811
Patent No. 6482936
GENERAL INFORMATION:
APPLICANT: HU, Song et al

; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-835-811-1

Query Match 5.8%; Score 130.6; DB 3; Length 1696;
Best Local Similarity 93.8%; Pred. No. 1.8e-18;
Matches 136; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 2117 CTCTTTAATGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2176
Db 1501 CACTGTATAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1560
Qy 2177 AA 2236
Db 1561 AA 1620
Qy 2237 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db 1621 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1645

Search completed: May 29, 2006, 12:38:41
Job time : 724 secs

Db 181 CGAGCCAGTTCCGGGTGTCCGGCTGGATCGGAACCTGGAACTGGGGCGAGACATGGAGC 240
Qy 241 TGAAGTGCCAGGTGCTGCTGTCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 300
Db 241 TGAAGTGCCAGGTGCTGCTGTCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGC 300
Qy 301 GCGGCGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAAACAGCCCAAGGGG 360
Db 301 GCGGCGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAAACAGCCCAAGGGG 360
Qy 361 CCGAGGGGCTGGACACCGAGGTTCTCGGCGAGAGGTTGGGGGACACCTTCGTCCTCA 420
Db 361 CCGAGGGGCTGGACACCGAGGTTCTCGGCGAGAGGTTGGGGGACACCTTCGTCCTCA 420
Qy 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Db 421 CCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACT 480
Qy 481 CCATCATGTACTTCCAGCCACTTCTGCGGCTCTTCTGCGGAGCGCCACACGACGC 540
Db 481 CCATCATGTACTTCCAGCCACTTCTGCGGCTCTTCTGCGGAGCGCCACACGACGC 540
Qy 541 CAGCGCGGACACCAACACCGGCGCCACCATCGCGTGCAGCGCTGTCCTGCGC 600
Db 541 CAGCGCGGACACCAACACCGGCGCCACCATCGCGTGCAGCGCTGTCCTGCGC 600
Qy 601 CAGAGGGTGCAGCGCGCGGGGCGCAGTGCACACGAGGGGCTGAGCTTCGCT 660
Db 601 CAGAGGGTGCAGCGCGCGGGGCGCAGTGCACACGAGGGGCTGAGCTTCGCT 660
Qy 661 GTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGCTCCTTCTCTGTCACGTG 720
Db 661 GTGATATCTACATCTGGGCGCCTTGGCGGGACTTGTGGGCTCCTTCTCTGTCACGTG 720
Qy 721 TTATCACCCTTACTGCAACACAGGACCAAGACGTTGTTGCAATGTCCCGGCTG 780
Db 721 TTATCACCCTTACTGCAACACAGGACCAAGACGTTGTTGCAATGTCCCGGCTG 780
Qy 781 TGGTCAAACTCGGAGACAAGCCAGCCTTTCGGGAGATACGCTAAACCTGTGCAACAG 840
Db 781 TGGTCAAACTCGGAGACAAGCCAGCCTTTCGGGAGATACGCTAAACCTGTGCAACAG 840
Qy 841 CCATCATATTAATCAACTGAGATCCTTCTTTTGGGAGGAGCAAGTCTTCCCTTTCAT 900
Db 841 CCATCATATTAATCAAACTGAGATCCTTCTTCTTTTGGGAGGCAAGTCTTCCCTTTCAT 900
Qy 901 TTTTTCAGTCTTCTCCCTGCTATTCATTTCTCATGATTATTTTGTAGTGGGGGGG 960
Db 901 TTTTTCAGTCTTCTCCCTGCTATTCATTTCTCATGATTATTTTGTAGTGGGGGGG 960
Qy 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTAC 1020
Db 961 GTGGGAAAGATTACTTTTCTTTATGTGTTTGAACGGGAAACAAACTAGGTAAATCTAC 1020
Qy 1021 AGTACACACAAGGTCACAATATGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGG 1080
Db 1021 AGTACACACAAGGTCACAATATGTTGTGCGCACATCGCGGTAGGCGGTGGAAGGG 1080
Qy 1081 CAGGCGAGCTACCCGAGAGTTCTCAGATCATGCTGAGAGAGCTGGAGGCCCAATG 1140
Db 1081 CAGGCGAGCTACCCGAGAGTTCTCAGATCATGCTGAGAGAGCTGGAGGCCCAATG 1140
Qy 1141 CCATCTCAACCTCTTCCCGCGCGTTTACAAAGGGGAGGCTAAAGCCCGAGAGACGCT 1200
Db 1141 CCATCTCAACCTCTTCCCGCGCGTTTACAAAGGGGAGGCTAAAGCCCGAGAGACGCT 1200
Qy 1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
Db 1201 TGATCAAAAGGCACACAGCAAGTCAAGGTTGAGCAGTAGCTGGAGGACCTTGTCTCCA 1260
Qy 1261 GCTCAGGCTCTTTCCTCACACCACTTCTTCTTCCGAGGCGCTTCTCAGGG 1320
Db 1261 GCTCAGGCTCTTTCCTCACACCACTTCTTCTTCTTCCGAGGCGCTTCTCAGGG 1320

Qy 1321 TGAGGTCTTGAAGTCTCCAAACGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 1380
Db 1321 TGAGGTCTTGAAGTCTCCAAACGCAAGGAAACAAGTACTTCTTGATACCTGGGATCTGT 1380
Qy 1381 GCCCAGAGCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCTTTGGCAGAGTCTTAT 1440
Db 1381 GCCCAGAGCTCGAGGAGGTAATGAATTAAGAAGAGAACTGCTTTGGCAGAGTCTTAT 1440
Qy 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAAATGTATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATAATCAAGCCCTAAAATGTATAGACCTAA 1500
Qy 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTGGAAAATGAATCCCTCTATCTCTTAAAGAAAT 1560
Db 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTGGAAAATGAATCCCTCTATCTCTTAAAGAAAT 1560
Qy 1561 CTCTGTAAACCCCTATGTGGAGCGGAATTTGCTCTCCAGCCCTTGCAITTCAGAGGG 1620
Db 1561 CTCTGTAAACCCCTATGTGGAGCGGAATTTGCTCTCCAGCCCTTGCAITTCAGAGGG 1620
Qy 1621 CCCATGAAGAGGACAGCTACCCCTTTACAAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGCTACCCCTTTACAAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Qy 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAAATGCTCTGGATCACTGATGA 1740
Db 1681 CTAAAGCCCTCTTGAATCTCTGAATTTGAGATACAAAATGCTCTGGATCACTGATGA 1740
Qy 1741 CTTTTTATCTTTTGAAGCAATTTGTTGGAGGCCCTCACAGCCCTGCGCTCTGCT 1800
Db 1741 CTTTTTATCTTTTGAAGCAATTTGTTGGAGGCCCTCACAGCCCTGCGCTCTGCT 1800
Qy 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Db 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGCCCAA 1860
Qy 1861 CTGCTGTCCCAACATGCACTTCTGCTTAAAGGTATGTTTAAAGCAATGCTGCGCAT 1920
Db 1861 CTGCTGTCCCAACATGCACTTCTGCTTAAAGGTATGTTTAAAGCAATGCTGCGCAT 1920
Qy 1921 GGAGAGAAACCTTAAGTAGATAGGAAATAGAACCACTCATATTTCTTCCCTTAGG 1980
Db 1921 GGAGAGAAACCTTAAGTAGATAGGAAATAGAACCACTCATATTTCTTCCCTTAGG 1980
Qy 1981 AATAATCTCTGTTAATATGTTGATACATTTCTCTGATTTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATACATTTCTCTGATTTTCTACACATACATGTA 2040
Qy 2041 AATAATCTTTTAAATAGGGTGTACTATGCTGTTATGAGTGGCTTTAATGAT 2100
Db 2041 AATAATCTTTTAAATAGGGTGTACTATGCTGTTATGAGTGGCTTTAATGAT 2100
Qy 2101 AAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAAAGGAAAAA 2160
Db 2101 AAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAAAGGAAAAA 2160
Qy 2161 AAA 2220
Db 2161 AAA 2220
Qy 2221 AAA 2261
Db 2221 AAA 2261

RESULT 2
US-10-888-313A-99
; Sequence 99, Application US/10888313A
; Publication No. US20050100934A1
; GENERAL INFORMATION:
; APPLICANT: LEE, Kevin
; APPLICANT: AXEL, Richard

APPLICANT: STRAPPS, Walter
APPLICANT: BARNEA, Gilad
TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction
FILE REFERENCE: SENTI 203.2
CURRENT APPLICATION NUMBER: US/10/888,313A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/566,113
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60/511,918
PRIOR FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/485,968
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 101
SEQ ID NO 99
LENGTH: 2261
TYPE: DNA
ORGANISM: homo sapiens
US-10-888-313A-99

Query Match 100.0%; Score 2261; DB 10; Length 2261;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCAGGCTCCGGCCGGCGGAGGCGCAACTTCCCTCGGGCCCCCAACCGGCT 60
DB 1 GAATCAGGCTCCGGCCGGCGGCGGAGGCGCAACTTCCCTCGGGCCCCCAACCGGCT 60

QY 61 CCGCGCGGCTCCCTCGGGCCCGGAGCTTCGAGCCAAAGCAGCGTCTCGGGGAGCGGTCA 120
DB 61 CCGCGCGGCTCCCTCGGGCCCGGAGCTTCGAGCCAAAGCAGCGTCTCGGGGAGCGGTCA 120

QY 121 TGGCCTTACAGTACCGGCTTGTCTCTGCGGCTGCTGTGTCTTCCACGCCGACGAC 180
DB 121 TGGCCTTACAGTACCGGCTTGTCTCTGCGGCTGCTGTGTCTTCCACGCCGACGAC 180

QY 181 CGAGCCAGTTCGGGTGTCGCGCTGATCGACCTGGAACCTGGGCGAGACAGTGGAGC 240
DB 181 CGAGCCAGTTCGGGTGTCGCGCTGATCGACCTGGAACCTGGGCGAGACAGTGGAGC 240

QY 241 TGAAGTGCCAGGTGCTGTCTCAACCCGAGCTCGGGCTGCTGTGGCTTTCAGCCGC 300
DB 241 TGAAGTGCCAGGTGCTGTCTCAACCCGAGCTCGGGCTGCTGTGGCTTTCAGCCGC 300

QY 301 GCGCGCGCGCCAGTCCACTTCTCTTATACCTCTCCAAACCAAGCCCAAGCGG 360
DB 301 GCGCGCGCGCCAGTCCACTTCTCTTATACCTCTCCAAACCAAGCCCAAGCGG 360

QY 361 CCGAGGGCTGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCCTCA 420
DB 361 CCGAGGGCTGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCCTCA 420

QY 421 CCTCAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCACT 480
DB 421 CCTCAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCACT 480

QY 481 CCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCGAGGAGCCACACGAGCG 540
DB 481 CCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCGAGGAGCCACACGAGCG 540

QY 541 CAGCGCGGGACCAACACACCGGGCCCAACATCGGTGCGAGCCCTGTCCCTGCGCC 600
DB 541 CAGCGCGGGACCAACACACCGGGCCCAACATCGGTGCGAGCCCTGTCCCTGCGCC 600

QY 601 CAGGGCTGCGGCGAGCGGGGGCGAGTGCACACGAGGGGCTGAGCTTCGCT 660
DB 601 CAGGGCTGCGGCGAGCGGGGGCGAGTGCACACGAGGGGCTGAGCTTCGCT 660

QY 661 GTGATATCTACATCTGGGCGGCTTGGCGGAGCTTGTGGGTCTCTCTGTCACCTGG 720
DB 661 GTGATATCTACATCTGGGCGGCTTGGCGGAGCTTGTGGGTCTCTCTGTCACCTGG 720

QY 721 TTATCACCCTTTACTGCAACCAACAGAACCGAGACGTTTTCGCAAAATGTCCCGGCTG 780

DB 721 TTATCACCCTTTACTGCAACCAACAGAACCGAAGACGTGTGTTCGCAAAATGTCCCGCCTG 780
QY 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTCGGCGAGATACGTCTAACCTGTGCAACAG 840
DB 781 TGGTCAAAATCGGGAGACAAAGCCAGCTTTCGGCGAGATACGTCTAACCTGTGCAACAG 840
QY 841 CCATCATGTACTTCAAACTGAGATCCTTCTTTTGGGGGAGCAAGTCTTCCCTTCAT 900
DB 841 CCATCATGTACTTCAAACTGAGATCCTTCTTCTTTTGGGGGAGCAAGTCTTCCCTTCAT 900
QY 901 TTTTTCAGTCTTCTCCTGCTGATTCATCTCATGATTAATTTTATAGTGGGGCGG 960
DB 901 TTTTTCAGTCTTCTCCTGCTGATTCATCTCATGATTAATTTTATAGTGGGGCGG 960
QY 961 GTGGGAAAGATTACTTTTTTCTTTATGTGTTCGCGGAAACAAACTAGTAAAACTTAC 1020
DB 961 GTGGGAAAGATTACTTTTTTCTTTATGTGTTCGCGGAAACAAACTAGTAAAACTTAC 1020
QY 1021 AGTACACCAAGGCTCAATACTGTGTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 1080
DB 1021 AGTACACCAAGGCTCAATACTGTGTGTGCGCAATCGCGGTAGGGCGTGGAAAGGG 1080
QY 1081 CAGGCGAGGCTACCGCGAGAGTTCTCAGAATCATGCTGAGAGCTGAGAGGACCCATG 1140
DB 1081 CAGGCGAGGCTACCGCGAGAGTTCTCAGAATCATGCTGAGAGCTGAGAGGACCCATG 1140
QY 1141 CCATCTCAACCTTCTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT 1200
DB 1141 CCATCTCAACCTTCTCCCGCCGCTTTTACAAAGGGGAGGCTAAAGCCACAGACAGCT 1200
QY 1201 TGATCAAAAGGCAACAGCAAGTCAAGGTGAGAGTAGTACGTGAGGAGCCTTGTCTCCA 1260
DB 1201 TGATCAAAAGGCAACAGCAAGTCAAGGTGAGAGTAGTACGTGAGGAGCCTTGTCTCCA 1260
QY 1261 GCTCAGGCTCTTCTCCTCCACCACTCAGGTCTTCTTCCGAGGCCCTGCTCAGGG 1320
DB 1261 GCTCAGGCTCTTCTCCTCCACCACTCAGGTCTTCTTCCGAGGCCCTGCTCAGGG 1320
QY 1321 TGAGGTGCTTGAAGTCCAAAGGCAAGGAAACAGTACTTCTTGATACCTGGGATCTGT 1380
DB 1321 TGAGGTGCTTGAAGTCCAAAGGCAAGGAAACAGTACTTCTTGATACCTGGGATCTGT 1380
QY 1381 GCCAGAGCCTCGAGGAGGTAAATGAATTAAGAAGAGAACTGCTTTCGAGAGTCTAT 1440
DB 1381 GCCAGAGCCTCGAGGAGGTAAATGAATTAAGAAGAGAACTGCTTTCGAGAGTCTAT 1440
QY 1441 AATGTAAACAATATACAGACTTTTCTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1500
DB 1441 AATGTAAACAATATACAGACTTTTCTTTTATTAATCAAGCTTAAATTTGTATAGACCTAA 1500
QY 1501 AATAAATGAAGTGTGAGCTTAACTCGGAAATGAAATCCCTCTATCTCTAAAGAAAT 1560
DB 1501 AATAAATGAAGTGTGAGCTTAACTCGGAAATGAAATCCCTCTATCTCTAAAGAAAT 1560
QY 1561 CTCTGTGAAACCCCTATGTGAGGCGGAAATGCTCTCCAGGCCCTTGCAATTCAGAGGG 1620
DB 1561 CTCTGTGAAACCCCTATGTGAGGCGGAAATGCTCTCCAGGCCCTTGCAATTCAGAGGG 1620
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1680
DB 1621 CCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAAATTTGAGCATCAGTGAAGTTAAA 1680
QY 1681 CTAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA 1740
DB 1681 CTAGGCCCTCTTGAATCTCTGAAATTTGAGATACAAACATGTTCTGGGATCAGTGATGA 1740
QY 1741 CTTTATTACTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCACACAGCCCTGSCCTCTGT 1800
DB 1741 CTTTATTACTTTGTAAAGACAAATTTGTTGGAGAGCCCTTCACACAGCCCTGSCCTCTGT 1800
QY 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860
DB 1801 CAATAGCAGATACAGGATGAGGACAGCTGACTCTCTTAAGGAGGCTGAGAGGCCAAA 1860

| | | | |
|----|------|--|------|
| QY | 421 | CCCTGAGCGACTTCCGCCGAGAGAAAGGGGCTACTATTTCTGCTCGGCCCTGAGCAACT | 480 |
| DB | 421 | | |
| QY | 481 | CCCTGAGCGACTTCCGCCGAGAGAAAGGGGCTACTATTTCTGCTCGGCCCTGAGCAACT | 480 |
| DB | 481 | | |
| QY | 541 | CCATCATGTACTTTCAGGCCACTTTCGTGCCGGTCTTCCTGCGAGCGAAGCCACACGACGC | 540 |
| DB | 541 | CCATCATGTACTTTCAGGCCACTTTCGTGCCGGTCTTCCTGCGAGCGAAGCCACACGACGC | 540 |
| QY | 601 | CAGCGCCGGACCAACCAACGCGGCCCAACATCGCGTGCAGGCCCTGTCCCTGGGCC | 600 |
| DB | 601 | CAGCGCCGGACCAACCAACGCGGCCCAACATCGCGTGCAGGCCCTGTCCCTGGGCC | 600 |
| QY | 661 | CAGAGCGCTGCCGCCAGCGCGGGGGCGCAGTGCAACAGAGGGGGCTGGACTTCCGCT | 660 |
| DB | 661 | CAGAGCGCTGCCGCCAGCGCGGGGGCGCAGTGCAACAGAGGGGGCTGGACTTCCGCT | 660 |
| QY | 721 | GTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTCACTGG | 720 |
| DB | 721 | | |
| QY | 781 | TTATCACCCCTTACTGCAACACAGGAACCGAAGCGTGTGTAATGTCCCGGGCTG | 780 |
| DB | 781 | | |
| QY | 841 | TGCTCAAAATCGGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG | 840 |
| DB | 841 | TGCTCAAAATCGGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCTAACCCCTGTGCAACAG | 840 |
| QY | 901 | CCACTACATTACTTCAAACCTGAGATCCTTCTTTTGAGGGAGCAAGTCTTCCCTTTTCAT | 900 |
| DB | 901 | CCACTACATTACTTCAAACCTGAGATCCTTCTTTTGAGGGAGCAAGTCTTCCCTTTTCAT | 900 |
| QY | 961 | TTTTCCTCAGTCTTCTCCCTGTGTATTCATTCATGATTAATTAATTTAGTGGGGGGGG | 960 |
| DB | 961 | TTTTCCTCAGTCTTCTCCCTGTGTATTCATTCATGATTAATTAATTTAGTGGGGGGGG | 960 |
| QY | 1021 | GTGGAAAGATTACTTTTTCCTTATGTGTTGACGGGAACAAAACTAGGTAAAATCTAC | 1020 |
| DB | 1021 | GTGGAAAGATTACTTTTTCCTTATGTGTTGACGGGAACAAAACTAGGTAAAATCTAC | 1020 |
| QY | 1081 | AGTACACCAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCTGGAAAGGGG | 1080 |
| DB | 1081 | AGTACACCAAGGGTCACAATACTGTTGTGCGCACATCGCGGTAGGGCTGGAAAGGGG | 1080 |
| QY | 1141 | CAGGCCAGAGTACCCGCGAGTCTCAGAAATCATGTGTGAGAGAGCTGGAGGACCCCATG | 1140 |
| DB | 1141 | CAGGCCAGAGTACCCGCGAGTCTCAGAAATCATGTGTGAGAGAGCTGGAGGACCCCATG | 1140 |
| QY | 1201 | CCATCTCAACCTCTTCCCGGCCGTTTTTACAAAGGGGGAGGCTTAAAGCCACAGAGACAGCT | 1200 |
| DB | 1201 | CCATCTCAACCTCTTCCCGGCCGTTTTTACAAAGGGGGAGGCTTAAAGCCACAGAGACAGCT | 1200 |
| QY | 1261 | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCA | 1260 |
| DB | 1261 | TGATCAAAAGGCACACAGCAAGTCAAGGTTGGAGCAGTAGCTGGAGGGACCTTGTCTCCCA | 1260 |
| QY | 1321 | GCTCAGGGCTCTTTCCTCCACACATTCAGGTCTTCTTTCCGAGGGCCCTGTCTCAGGG | 1320 |
| DB | 1321 | GCTCAGGGCTCTTTCCTCCACACATTCAGGTCTTCTTTCCGAGGGCCCTGTCTCAGGG | 1320 |
| QY | 1381 | TGAGGTGCTTGAGTCTCCACCGGCACAGGAAACAGTACTCTTGTATACCTGGGATCTGT | 1380 |
| DB | 1381 | TGAGGTGCTTGAGTCTCCACCGGCACAGGAAACAGTACTCTTGTATACCTGGGATCTGT | 1380 |
| QY | 1441 | GCCCAGAGCCTCGAGGAGTAAATGAAATTAAGAGAGAGACTGCGCTTTGGCAGAGTTCTAT | 1440 |
| DB | 1441 | GCCCAGAGCCTCGAGGAGTAAATGAAATTAAGAGAGAGACTGCGCTTTGGCAGAGTTCTAT | 1440 |
| QY | 1501 | AATGTAACAATATCAGACTTTTTTTTTTTTATTAATCAAGCCATAAATGTATAGACTAA | 1500 |
| DB | 1501 | AATGTAACAATATCAGACTTTTTTTTTTTTATTAATCAAGCCATAAATGTATAGACTAA | 1500 |

[illegible]

RESULT 6

US-10-804-763-4
; Sequence 4, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/ITAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens

QY 2101 AAACATTTGTAGCATCTCTTAATGGGTAACAGCAAAAAAAAAAAAAAAAAAAAA 2160
DB 1990 AAACATTTGTAGCATCTCTTAATGGGTAACAGCAAAAAAAAAAAAAAAAAAAAA 2049
QY 2161 AA 2220
DB 2050 AA 2109
QY 2221 AA 2261
DB 2110 AA 2150

RESULT 7
US-10-723-860-1243
; Sequence 1243, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193 NPU01
; CURRENT APPLICATION NUMBER: US/10/723,860
; PRIOR FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1243
; LENGTH: 1729
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1243

Query Match 60.2%; Score 1361.4; DB 9; Length 1729;
Best Local Similarity 99.2%; Pred. No. 2.3e-209;
Matches 1368; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 759 GTTTCGAATGTCCTCCCGCTGTGCTCAATCGGAGACAGCCAGCTTTCGGCGAGA 818
DB 287 GCTTTCCTCTCTTCAGGCGCTGTGCTCAATCGGAGACAGCCAGCCGCTTTCGGCGAGA 346
QY 819 TACGCTCAACCTGTGCAACAGCCACTACATTAATCTCAAACTGAGATCTCTCTTTTCGAG 878
DB 347 TACGCTCAACCTGTGCAACAGCCACTACATTAATCTCAAACTGAGATCTCTCTTTTCGAG 406
QY 879 GGAGCAAGTCTCTCCCTTTTCATTTTTCAGTCTTCCCTGCTGTAATTCATTCATGA 938
DB 407 GGAGCAAGTCTCTCCCTTTTCATTTTTCAGTCTTCCCTGCTGTAATTCATTCATGA 466
QY 939 TTATTTATTTAGTGGGGGGGGTGGGAAAGATTAATTTTCTTTTATGTTTTCAGCGGA 998
DB 467 TTATTTATTTAGTGGGGGGGGTGGGAAAGATTAATTTTCTTTTATGTTTTCAGCGGA 526
QY 999 AACAAAACCTAGGTAAATCTACAGTACACCAAGGGTCACAATATCTGTTGCGCACAT 1058
DB 527 AACAAAACCTAGGTAAATCTACAGTACACCAAGGGTCACAATATCTGTTGCGCACAT 586
QY 1059 CGCGTAGGGCGTGAAGAGGGGCGAGCGAGCTACCGCGAGAGTTCTCAGAAATCATGCT 1118
DB 587 CGCGTAGGGCGTGAAGAGGGGCGAGCGAGCTACCGCGAGAGTTCTCAGAAATCATGCT 646
QY 1119 CAGAGAGCTGGAGGACCCATCGCATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGGG 1178
DB 647 CAGAGAGCTGGAGGACCCATCGCATCTCAACCTCTTCCCGCCGCTTTTACAAAGGGGG 706
QY 1179 AGGCTAAAGCCAGAGACAGCTTTGATCAAGGSCACACAGAGTTCAGGTTGGACAGTA 1238
DB 707 AGGCTAAAGCCAGAGACAGCTTTGATCAAGGSCACACAGAGTTCAGGTTGGACAGTA 766
QY 1239 GCTGGAGGAGCCTTGTCTCCAGCTCAGGGCTCTTTCTCCACACCATTCAGGCTCTTCT 1298

DB 767 GCTGGAGGAGCCTTGTCTCCAGCTCAGGGCTCTTTCCTCCACACCATTCAGGCTCTTCT 826
QY 1299 TTCCGAGGCCCTGTCTCAGGGTGAAGTCTTGAAGTCTTCCACGCGCAGGGAACAGTAC 1358
DB 827 TTCCGAGGCCCTGTCTCAGGGTGAAGTCTTGAAGTCTTCCACGCGCAGGGAACAGTAC 886
QY 1359 TTCTTGATACCTGGGATACCTGTGCCAGAGCCTCGAGGAGTAAATGAATTAAGAGAGAGA 1418
DB 887 TTCTTGATACCTGGGATACCTGTGCCAGAGCCTCGAGGAGTAAATGAATTAAGAGAGAGA 946
QY 1419 ACTGCTTTGGCAGAGTTCTATAATGTAAACAAATATCAGACTTTTTTTTTTATAATCAA 1478
DB 947 ACTGCTTTGGCAGAGTTCTATAATGTAAACAAATATCAGACTTTTTTTTTTATAATCAA 1006
QY 1479 GCCTAAAAATGTATAGACTTAAATATAAGTGGTGAAGTCTTAACCCCTCGGAAATGAA 1538
DB 1007 GCCTAAAAATGTATAGACTTAAATATAAGTGGTGAAGTCTTAACCCCTCGGAAATGAA 1066
QY 1539 TCCCTCTATCTCTAAAGAAAAATCTCTGTGAACCCCTATGTGGAGCGGAAATTCCTCTCC 1598
DB 1067 TCCCTCTATCTCTAAAGAAAAATCTCTGTGAACCCCTATGTGGAGCGGAAATTCCTCTCC 1126
QY 1599 CAGCCCTTGCATTGACAGAGGGGCCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAA 1658
DB 1127 CAGCCCTTGCATTGACAGAGGGGCCCATGAAGAGGACAGGCTACCCCTTTTACAAATAGAA 1186
QY 1659 TTTGAGCATCAGTGAAGTTAACTAAAGCCCTCTTGAATCTCTGAATTTGAGATCAAAAC 1718
DB 1187 TTTGAGCATCAGTGAAGTTAACTAAAGCCCTCTTGAATCTCTGAATTTGAGATCAAAAC 1246
QY 1719 ATGTTCTGGGATCAGTCACTGATCACTTTTATATCTTTGTAAGACAAATTTGTTGAGAGCCCC 1778
DB 1247 ATGTTCTGGGATCAGTCACTGATCACTTTTATATCTTTGTAAGACAAATTTGTTGAGAGCCCC 1306
QY 1779 TCACACAGCCCTGGCTCTGCTCAACTAGCAGATACAGGGATGAGGAGACCTGACTCTC 1838
DB 1307 TCACACAGCCCTGGCTCTGCTCAACTAGCAGATACAGGGATGAGGAGACCTGACTCTC 1366
QY 1839 TTAAGGAGCTGAGAGCCCAACTGCTCTCCCAACATGCACTTCTTCTGCTTAAAGGTATG 1898
DB 1367 TTAAGGAGCTGAGAGCCCAACTGCTCTCCCAACATGCACTTCTTCTGCTTAAAGGTATG 1426
QY 1899 GTACAAGCAATGCTCTGCTTGGAGAGAAAAAACTTAAGTAGATAAGGAAATAAGAAC 1958
DB 1427 GTACAAGCAATGCTCTGCTTGGAGAGAAAAAACTTAAGTAGATAAGGAAATAAGAAC 1486
QY 1959 ACTCATAATCTTCACTTAGGAAATACTCTGTTAATATGTTGATCATTTCTCTGAT 2018
DB 1487 ACTCATAATCTTCACTTAGGAAATACTCTGTTAATATGTTGATCATTTCTCTGAT 1546
QY 2019 TATTTTCTACATACATGTAATAATATCTCTTTTAAATAGGCTGTACTATGCT 2078
DB 1547 TATTTTCTACATACATGTAATAATATCTCTTTTAAATAGGCTGTACTATGCT 1606
QY 2079 GTTATGAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGTAAACAGCA 2137
DB 1607 GTTATGAGTGGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGTAAACAGCA 1665

RESULT 8
US-10-207-655-173
; Sequence 173, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 173
; LENGTH: 1060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-173

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Query Match 46.4%; Score 1048; DB 6; Length 1060;
Best Local Similarity 100.0%; Pred. No. 5.6e-159;
Matches 1048; Conservative 0; Mismatches 0; Indels 0

| | | | |
|----|-----|---|------|
| Qy | 67 | CGCCTCCCTCGCGCCCGAGGTTTCGAGCCAAAGACGCTCTCTGGGGAGCGGTCAATGCGCT | 126 |
| Db | 13 | CGCCTCCCTCGCGCCCGAGGTTTCGAGCCAAAGACGCTCTCTGGGGAGCGGTCAATGCGCT | 72 |
| Qy | 127 | TACAGTGACCGCCTCTCTCTCGCGCTTGGCTTGTCTCTCCAGCCGCGCAGGCGCGAGCC | 186 |
| Db | 73 | TACAGTGACCGCCTTGTCTCTGCGCTTGGCTTGTCTCTCCAGCCGCGCAGGCGCGAGCC | 132 |
| Qy | 187 | AGTTTCCGGGTGTTCGCGCTGAGTACGAGACCTTGGAACTCTGGGCGAGACAGTGGAGCTGAAGT | 246 |
| Db | 133 | AGTTTCCGGGTGTTCGCGCTGAGTACGAGACCTTGGAACTCTGGGCGAGACAGTGGAGCTGAAGT | 192 |
| Qy | 247 | GCCAGTGTCTGTGTCTCAAAACCCGAGCTGGGCTCTCTCGTGTCTTTCAGCGCGCGCGCG | 306 |
| Db | 193 | GCCAGTGTCTGTGTCTCAAAACCCGAGCTGGGCTCTCTCGTGTCTTTCAGCGCGCGCGCG | 252 |
| Qy | 307 | CGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGGCGCCGAGG | 366 |
| Db | 253 | CGCGCGCAGTCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGGCGCCGAGG | 312 |
| Qy | 367 | GGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTTGGGGGACACCTTCTCTCAACCTCTGA | 426 |
| Db | 313 | GGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTTGGGGGACACCTTCTCTCAACCTCTGA | 372 |
| Qy | 427 | GCAGCTTTCGCGCGAGAGAAAGAGGGCTACTATTTCTGTCTGGCCCTGAGCAACTTCATCA | 486 |
| Db | 373 | GCAGCTTTCGCGCGAGAGAAAGAGGGCTACTATTTCTGTCTGGCCCTGAGCAACTTCATCA | 432 |
| Qy | 487 | TGTACTTTCAGCCACTTCGTGCGCGCTCTCTCGCCAGCGAGAGCCACCAAGCGCCAGCGC | 546 |
| Db | 433 | TGTACTTTCAGCCACTTCGTGCGCGCTCTCTCGCCAGCGAGAGCCACCAAGCGCCAGCGC | 492 |
| Qy | 547 | CGCGACCAACCAACCGCGCGCCACCATTCGCTCGCAGCCCTTCTCCTTGGCGCCAGAGG | 606 |
| Db | 493 | CGCGACCAACCAACCGCGCGCCACCATTCGCTCGCAGCCCTTCTCCTTGGCGCCAGAGG | 552 |
| Qy | 607 | CGTCCGCGCCACGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTTCGCTGTGTGATA | 666 |
| Db | 553 | CGTCCGCGCCACGCGCGGGGGCGAGTGCACACGAGGGGCTGGACTTTCGCTGTGTGATA | 612 |
| Qy | 667 | TCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCCTCTCTCTCACTGGTTATCA | 726 |
| Db | 613 | TCTACATCTGGGCGCCCTTGGCCGGGACTTGTGGGGTCCCTCTCTCTCACTGGTTATCA | 672 |
| Qy | 727 | CCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAAATGTCGCCGGCTGTGGTCA | 786 |
| Db | 673 | CCCTTTACTGCAACACACAGGAACCGAAGACGTGTTTGCAAAATGTCGCCGGCTGTGGTCA | 732 |
| Qy | 787 | AATCGGGAGACAAGCCACGACCTTTTCGGCGAGATACGTCTAACCTGTGTGCAACAGCCACTA | 846 |
| Db | 733 | AATCGGGAGACAAGCCACGACCTTTTCGGCGAGATACGTCTAACCTGTGTGCAACAGCCACTA | 792 |
| Qy | 847 | CATTACTTCAAACTGAGATCCCTTCCTTTTGGAGGAGCAGTCCCTTCCCTTTCATTTTTTTC | 906 |
| Db | 793 | CATTACTTCAAACTGAGATCCCTTCCTTTTGGAGGAGCAGTCCCTTCCCTTTCATTTTTTTC | 852 |
| Qy | 907 | CAGTCTTCTCCCTCTGTGTATTCAATTCATCATATTATTATTATTAGTGGGGCGGGTGGGA | 966 |
| Db | 853 | CAGTCTTCTCCCTCTGTGTATTCAATTCATCATATTATTATTATTAGTGGGGCGGGTGGGA | 912 |
| Qy | 967 | AAGATTACTTTTTCTTTATGTTTGAACGGGAAAACAAACCTAGGTAATAATCTACAGTACA | 1026 |
| Db | 913 | AAGATTACTTTTTCTTTATGTTTGAACGGGAAAACAAACCTAGGTAATAATCTACAGTACA | 972 |

Db 133 AGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAGCTGAAGT 192
QY 247 GCCAGGTGCTGTGTCCTCAACCCGACGCTCGGGCTGCTGCTGGCTTCCAGCCGCGGGG 306
Db 193 GCCAGGTGCTGTGTCCTCAACCCGACGCTCGGGCTGCTGCTGGCTTCCAGCCGCGGGG 252
QY 307 CGCGCCGAGTCCACCTTCTCTCTATACCTTCTCCAAACAAAGCCCAAGGGCGCGAGG 366
Db 253 CGCGCCGAGTCCACCTTCTCTCTATACCTTCTCCAAACAAAGCCCAAGGGCGCGAGG 312
QY 367 GCTGTGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCCTCCACCTCA 426
Db 313 GCTGTGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCCTCCACCTCA 372
QY 427 GCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTCGAGCAACTCCATCA 486
Db 373 GCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTCGAGCAACTCCATCA 432
QY 487 TGTAATTAGCCACTTGTGCGGGTCTTCTGCGAGGAAGCCACACGAGCCGAGCGC 546
Db 433 TGTACTTCAGCCACTTGTGCGGGTCTTCTGCGAGGAAGCCACACGAGCCGAGCGC 492
QY 547 CGCGACCAACACCGCGGCCACCATCGCTCGGAGCCCTGCTCCCTCGCGCCGAGGG 606
Db 493 CGCGACCAACACCGCGGCCACCATCGCTCGGAGCCCTGCTCCCTCGCGCCGAGGG 552
QY 607 CGTCCGGCGCAGCGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCTGTGATA 666
Db 553 CGTCCGGCGCAGCGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCTGTGATA 612
QY 667 TCTACATCTGGCGGCTTGGCGGGGACTTGTGGGGTCTTCTCTGCTCACTGGTTATCA 726
Db 613 TCTACATCTGGCGGCTTGGCGGGGACTTGTGGGGTCTTCTCTGCTCACTGGTTATCA 672
QY 727 CCTTTTACTGCAACACACAGGACCGAGACGTTTGGCAATGTCCCGGCTGTGGTCA 786
Db 673 CCTTTTACTGCAACACACAGGACCGAGACGTTTGGCAATGTCCCGGCTGTGGTCA 732
QY 787 AATCGGAGACAAGCCGACCTTTTCGGGAGATAGTCTAAACCTGTGCAACGACACTA 846
Db 733 AATCGGAGACAAGCCGACCTTTTCGGGAGATAGTCTAAACCTGTGCAACGACACTA 792
QY 847 CATTAATTCAACTGAGATCTTCTTTTGGGAGCAAGTCTTCCCTTTCAATTTTTC 906
Db 793 CATTAATTCAACTGAGATCTTCTTTTGGGAGCAAGTCTTCCCTTTCAATTTTTC 852
QY 907 CAGTCTTCTCCTGTGATTCATTTCTCATGATTATTTTGTGGGGCGGGTGGGA 966
Db 853 CAGTCTTCTCCTGTGATTCATTTCTCATGATTATTTTGTGGGGCGGGTGGGA 912
QY 967 AAGATTACTTTTCTTTTATGTGTTGACGGGAAACAAACTAGGTAAATCTACAGTCA 1026
Db 913 AAGATTACTTTTCTTTTATGTGTTGACGGGAAACAAACTAGGTAAATCTACAGTCA 972
QY 1027 CCACAAGGGTCAATATCTGTTGTGCGCATCTCGCGGTAGGGCTGGAAAGGGCGAGGCC 1086
Db 973 CCACAAGGGTCAATATCTGTTGTGCGCATCTCGCGGTAGGGCTGGAAAGGGCGAGGCC 1032
QY 1087 AGAGCTACCCGAGAGTTCTCAGATCA 1114
Db 1033 AGAGCTACCCGAGAGTTCTCAGATCA 1060

RESULT 10

US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransplantation
; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)

; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Query Match 31.3%; Score 708; DB 9; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.7e-104;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 ATGGCGCTTACCAAGTACCGGCTTGTCTGCTGCGCTGGCTTGTCTGCTCAGCGCGCAGG 179
Db 1 ATGGCGCTTACCAAGTACCGGCTTGTCTGCTGCGCTGGCTTGTCTGCTCAGCGCGCAGG 60
QY 180 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 120
QY 240 CTGAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGCTGCTGCTCTTCCAGCGG 299
Db 121 CTGAAGTGCAGGTGCTGTCTCCAAACCGACGTCGGGCTGCTGCTGCTCTTCCAGCGG 180
QY 300 CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAACAAAGCCCAAGGGG 359
Db 181 CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAACAAAGCCCAAGGGG 240
QY 360 GCCGAGGGGCTGCGACACCGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCTGCTC 419
Db 241 GCCGAGGGGCTGCGACACCGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCTGCTC 300
QY 420 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCGCTTGAGCAAC 360
QY 480 TCCATCATGTACTTACGACCATCTGTCGGGCTTCTGCGGAGCGGAGCCACCGAGCG 539
Db 361 TCCATCATGTACTTACGACCATCTGTCGGGCTTCTGCGGAGCGGAGCCACCGAGCG 420
QY 540 CCAGCGCGCGGACCAACACCGCGCCACCATCGCTGCGGAGCCCTGCTGCTGCGC 599
Db 421 CCAGCGCGCGGACCAACACCGCGCCACCATCGCTGCGGAGCCCTGCTGCTGCGC 480
QY 600 CCAGAGGGGCTGCGCGCGGCGCGGCGGCGCAGTGCGACACGAGGGGGTGGACTTCGCGC 659
Db 481 CCAGAGGGGCTGCGCGCGGCGCGGCGGCGCAGTGCGACACGAGGGGGTGGACTTCGCGC 540
QY 660 TGTGATATCATCTGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTG 719
Db 541 TGTGATATCATCTGCGGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACCTG 600
QY 720 GTTATCATCTTACTGCAACACGAGGAACCGAAGACGTTGTTGCAAAATGTCCTCGGCT 779
Db 601 GTTATCATCTTACTGCAACACGAGGAACCGAAGACGTTGTTGCAAAATGTCCTCGGCT 660
QY 780 GTGCTCAAAATCGGAGACAAGCCAGCCCTTTTCGGCGAGATAGTCTAA 827
Db 661 GTGCTCAAAATCGGAGACAAGCCAGCCCTTTTCGGCGAGATAGTCTAA 708

RESULT 11

US-10-804-763-28
; Sequence 28, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula

```
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-804-763-28

Query Match      31.3%; Score 708; DB 10; Length 708;
Best Local Similarity 100.0%; Pred. No. 2.7e-104;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 120 ATGGCCTTACAGTACCGCCTTGTCTCGCGCTGGCCTTGCTGCCACGCGCCGAGG 179
Db 1 ATGGCCTTACAGTACCGCCTTGTCTCGCGCTGGCCTTGCTGCCACGCGCCGAGG 60

Qy 180 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGGAACCTGGGGGAGACAGTGGAG 239
Db 61 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGGAACCTGGGGGAGACAGTGGAG 120

Qy 240 CTGAAGTGCCAGGTGCTGCTGTCCAAACCCGACGTGGGCTGCTCGTGCTCTTCCAGCG 299
Db 121 CTGAAGTGCCAGGTGCTGCTGTCCAAACCCGACGTGGGCTGCTCGTGCTCTTCCAGCG 180

Qy 300 CGCGGCGCGCGCGGACGTCACCTTCTCTATACCTCTCCGAAACCAAGCCCAAGCG 359
Db 181 CGCGGCGCGCGCGGACGTCACCTTCTCTATACCTCTCCGAAACCAAGCCCAAGCG 240

Qy 360 GCCGAGGGGTGGACACCCAGCGGTTCTCGGCGAAGAGTGGGGGACACCTTGTCTCTC 419
Db 241 GCCGAGGGGTGGACACCCAGCGGTTCTCGGCGAAGAGTGGGGGACACCTTGTCTCTC 300

Qy 420 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGGCCCTTGAGCAAC 479
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTGGGCCCTTGAGCAAC 360

Qy 480 TCCATATGTACTTACGACACTTCTGCGGGTCTTCCTGCGAGCGAAGCCACACGACG 539
Db 361 TCCATATGTACTTACGACACTTCTGCGGGTCTTCCTGCCAGCGAAGCCACACGACG 420

Qy 540 CCAGCGCGGACCAACCAACCGCGCCACCATCGGTCGCGAGCCCTGTCCCTGCGC 599
Db 421 CCAGCGCGGACCAACCAACCGCGCCACCATCGGTCGCGAGCCCTGTCCCTGCGC 480

Qy 600 CCAGAGGGGTGCGGCGCAGCGCGGGGGCGGAGTGCAACAGAGGGGCTGGACTTCGCC 659
Db 481 CCAGAGGGGTGCGGCGCAGCGCGGGGGCGGAGTGCAACAGAGGGGCTGGACTTCGCC 540

Qy 660 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCTG 719
Db 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCTG 600

Qy 720 GTTATCACCTTTACTGCAACCAACAGGAACCGAAGAGCTGTTTGCAAAATGTCGCCGCT 779
Db 601 GTTATCACCTTTACTGCAACCAACAGGAACCGAAGAGCTGTTTGCAAAATGTCGCCGCT 660

Qy 780 GTGTGCAAAATCGGGAGACAAAGCCAGCCCTTTTCGGGAGATAGTCTAA 827
Db 661 GTGTGCAAAATCGGGAGACAAAGCCAGCCCTTTTCGGGAGATAGTCTAA 708
```

RESULT 12
US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US2003018268A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.

```
; APPLICANT: Carboni, Joan M.  
; APPLICANT: Rowley, Ronald B.  
; APPLICANT: Wong, Tai W.  
; APPLICANT: Lee, Francis Y.  
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED  
; FILE REFERENCE: D0254 NP  
; CURRENT APPLICATION NUMBER: US/10/378,393  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/360,889  
; PRIOR FILING DATE: 2002-03-01  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 692  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-378-393-2

Query Match      30.6%; Score 692; DB 7; Length 692;  
Best Local Similarity 100.0%; Pred. No. 9.9e-102;  
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 AGCTTCGAGCCCAAGCAGGCTCTCGGGAGCGGTCATGSCCTTACCACTGACCGCTTGC 144  
Db 1 AGCTTCGAGCCCAAGCAGGCTCTCGGGAGCGGTCATGSCCTTACCACTGACCGCTTGC 60

Qy 145 TCCTGCGCTGGCCTTGTGCTCCACGCGCCAGGCCGAGCAGTTCCGGGTGTGCGCGC 204  
Db 61 TCCTGCGCTGGCCTTGTGCTCCACGCGCCAGGCCGAGCAGTTCCGGGTGTGCGCGC 120

Qy 205 TGGATCGGACCTGGAACCTGGGGCGAGACAGTGGAGCTGAAGTGCAGGTGTGCTGTCA 264  
Db 121 TGGATCGGACCTGGAACCTGGGGCGAGACAGTGGAGCTGAAGTGCAGGTGTGCTGTCCA 180

Qy 265 ACCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCGCGCGCGCGCTCCAGTCCACCT 324  
Db 181 ACCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGCGCGCGCGCGCTCCAGTCCACCT 240

Qy 325 TCCTCTATATCTCTCCCAAAACAAAGCCAAAGCGCGCGCGGGCTGGACACCCAGCGT 384  
Db 241 TCCTCTATATCTCTCCCAAAACAAAGCCAAAGCGCGCGCGGGCTGGACACCCAGCGT 300

Qy 385 TCTCGGCAAGAGGTGGGGGACACTTCTGCTCTCACTGAGGACCTTCCGCGGAGAGA 444  
Db 301 TCTCGGCAAGAGGTGGGGGACACTTCTGCTCTCACTGAGGACCTTCCGCGGAGAGA 360

Qy 445 ACAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCATGTACTTTCAGCCACTTCG 504  
Db 361 ACAGGGCTACTATTCTGCTCGGCCCTGAGCAACTCCATCATGTACTTTCAGCCACTTCG 420

Qy 505 TGCGGCTCTTCTGCGCAGGAAGCCACACGAGCGCGCGCGCGCGAGCAACCAACACCGG 564  
Db 421 TGCGGCTCTTCTGCGCAGGAAGCCACACGAGCGCGCGCGCGAGCAACCAACACCGG 480

Qy 565 CGCCCAACATCGCTCGCAGCGCCCTGTCTCTGCGCCGAGAGCGGTGCGCGCGCGCGCG 624  
Db 481 CGCCCAACATCGCTCGCAGCGCCCTGTCTCTGCGCCGAGAGCGGTGCGCGCGCGCGCG 540

Qy 625 GGGGCGCAGTGCACACGAGGGGGTGGACTTCGCTGTGATATCTACATCTGGGGGCCCT 684  
Db 541 GGGGCGCAGTGCACACGAGGGGGTGGACTTCGCTGTGATATCTACATCTGGGGGCCCT 600

Qy 685 TGGCGGGAATTGTGGGGTCTTCTCTGTGTCACTGGTTATCACCTTTATCTCAACACCA 744  
Db 601 TGGCGGGGACTTGTGGGGTCTTCTCTGTGTCACTGGTTATCACCTTTATCTCAACACCA 660

Qy 745 GGAACCGAAGAGTGTGCAAAATGTCGCCG 776  
Db 661 GGAACCGAAGAGTGTGCAAAATGTCGCCG 692
```

RESULT 13

US-10-378-393-6
; Sequence 6, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-6

Query Match 30.6%; Score 692; DB 7; Length 1995;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AGCTTCGAGCCAAGCAGCGTCTGGGAGCGGTCTATGCGCTTACGAGCGCGCTTGC 144
DB 18 AGCTTCGAGCCAAGCAGCGTCTGGGAGCGGTCTATGCGCTTACGAGCGCGCTTGC 77
QY 145 TCCTCCCGTGGCCTTGCTCTCCACGCCGCCAGCGCCAGCGAGTTCGCGGTGTGCCCGC 204
DB 78 TCCTCCCGTGGCCTTGCTCTCCACGCCGCCAGCGCCAGCGAGTTCGCGGTGTGCCCGC 137
QY 205 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 264
DB 138 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 197
QY 265 ACCCGACGTGGGCTGTCTTCCACGCCGCCAGCGCGCGCGCGCGCGCGCGCGCTTCC 324
DB 198 ACCCGACGTGGGCTGTCTTCCACGCCGCCAGCGCGCGCGCGCGCGCGCGCGCTTCC 257
QY 325 TCCTCTATACCTCTCCCAAAACAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 384
DB 258 TCCTCTATACCTCTCCCAAAACAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCC 317
QY 385 TCTCGGCAAGAGTGTGGGGACACCTTCGTCTCACTGAGCGACTTCCGCGGAGAGA 444
DB 318 TCTCGGCAAGAGTGTGGGGACACCTTCGTCTCACTGAGCGACTTCCGCGGAGAGA 377
QY 445 ACGAGGCTACTATTTCTGCTCGGCGCTGAGCACTCCATCATGTACTTACGCACTTGC 504
DB 378 ACGAGGCTACTATTTCTGCTCGGCGCTGAGCACTCCATCATGTACTTACGCACTTGC 437
QY 505 TGCCGGTCTTCTGCGAGGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
DB 438 TGCCGGTCTTCTGCGAGGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 497
QY 565 GCCCACCACATCGCGTCGAGCCCTGTCTCCGCGCCAGAGCGGTGCCGCGCGCGCGCG 624
DB 498 GCCCACCACATCGCGTCGAGCCCTGTCTCCGCGCCAGAGCGGTGCCGCGCGCGCGCG 557
QY 625 GGGGCGGAGTGCACAGAGGGGCTTGGACTTCCCTGTGATATCTACATCTGGGGCGCT 684
DB 558 GGGGCGGAGTGCACAGAGGGGCTTGGACTTCCCTGTGATATCTACATCTGGGGCGCT 617
QY 685 TGGCGGAGCTTGTGGGGTCTTCTCTGTCTACTGTTATCACCTTTACTTGCACACCA 744
DB 618 TGGCGGAGCTTGTGGGGTCTTCTCTGTCTACTGTTATCACCTTTACTTGCACACCA 677
QY 745 GGAACCGAGAGCGTGTGTTGCAAAATGTCGCCCG 776

DB 678 GGAACCGAGAGCGTGTGTTGCAAAATGTCGCCCG 709
RESULT 14
US-10-378-393-12
; Sequence 12, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-12

Query Match 30.5%; Score 690; DB 7; Length 690;
Best Local Similarity 100.0%; Pred. No. 2.1e-101;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AGCTTCGAGCCAAGCAGCGTCTGGGAGCGGTCTATGCGCTTACGAGCGCGCTTGC 144
DB 1 AGCTTCGAGCCAAGCAGCGTCTGGGAGCGGTCTATGCGCTTACGAGCGCGCTTGC 60
QY 145 TCCTCCCGTGGCCTTGCTCTCCACGCCGCCAGCGCCAGCGAGTTCGCGGTGTGCCCGC 204
DB 61 TCCTCCCGTGGCCTTGCTCTCCACGCCGCCAGCGCCAGCGAGTTCGCGGTGTGCCCGC 120
QY 205 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 264
DB 121 TGGATCGACCTGGAACTTGGGCGAGACAGTGGAGCTGAAGTGCAGAGTGTCTGTCCA 180
QY 265 ACCCGACGTGGGCTGTCTTCCACGCCGCCAGCGCGCGCGCGCGCGCGCGCTTCC 324
DB 181 ACCCGACGTGGGCTGTCTTCCACGCCGCCAGCGCGCGCGCGCGCGCGCTTCC 240
QY 325 TCCTCTATACCTCTCCCAAAACAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCTTCC 384
DB 241 TCCTCTATACCTCTCCCAAAACAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCTTCC 300
QY 385 TCTCGGCAAGAGTGTGGGGACACCTTCGTCTCACTGAGCGACTTCCGCGGAGAGA 444
DB 301 TCTCGGCAAGAGTGTGGGGACACCTTCGTCTCACTGAGCGACTTCCGCGGAGAGA 360
QY 445 ACGAGGCTACTATTTCTGCTCGGCGCTGAGCACTCCATCATGTACTTACGCACTTGC 504
DB 361 ACGAGGCTACTATTTCTGCTCGGCGCTGAGCACTCCATCATGTACTTACGCACTTGC 420
QY 505 TGCCGGTCTTCTGCGAGGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 564
DB 421 TGCCGGTCTTCTGCGAGGAGCCACACGAGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 565 GCCCACCACATCGCGTCGAGCCCTGTCTCCGCGCCAGAGCGGTGCCGCGCGCGCGCG 624
DB 481 GCCCACCACATCGCGTCGAGCCCTGTCTCCGCGCCAGAGCGGTGCCGCGCGCGCGCG 540
QY 625 GGGGCGGAGTGCACAGAGGGGCTTGGACTTCCCTGTGATATCTACATCTGGGGCGCT 684
DB 541 GGGGCGGAGTGCACAGAGGGGCTTGGACTTCCCTGTGATATCTACATCTGGGGCGCT 600

| | | | | | |
|----|-----|---------------|---------------------------------|---------------------|-----|
| Qy | 585 | TGGCCGGGAC | TGTGGGGTCTTCTTCCTGTCACTGGTTATCA | CCCTTTTACTGCAACCACA | 744 |
| Db | 601 | TGGCCGGGAC | TGTGGGGTCTTCTTCCTGTCACTGGTTATCA | CCCTTTTACTGCAACCACA | 660 |
| Qy | 745 | GGAAACCGAAGAC | GTGTTTGC | AAATGTC | 774 |
| Db | 661 | GGAAACCGAAGAC | GTGTTTGC | AAATGTC | 690 |

RESULT 15
US-10-378-393-10
; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

Query Match 30.5%; Score 690; DB 7; Length 2411;
Best Local Similarity 100.0%; Pred. No. 3.1e-101;
Matches 690; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| Qy | 85 | AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTATGGCCTTACAGTGAACCGCCTTGC | 144 |
| Db | 1 | AGCTTCGAGCCAAGCAGCGTCTCTGGGAGCGGTATGGCCTTACAGTGAACCGCCTTGC | 60 |
| Qy | 145 | TCCTGCCGCTGGCCTTGTCTCCACGCGCGCAGGCGCCAGTTCGCGGTGTGCGCGC | 204 |
| Db | 61 | TCCTGCCGCTGGCCTTGTCTCCACGCGCGCGAGCCAGTTCGCGGTGTGCGCGC | 120 |
| Qy | 205 | TGGATCGAGACCTGGAACTGTGGCGGAGACAGTGGAGCTGAAGTGCAGGTGCTGTCTCA | 264 |
| Db | 121 | TGGATCGAGACCTGGAACTGTGGCGGAGACAGTGGAGCTGAAGTGTGCTGTCTCA | 180 |
| Qy | 265 | ACCGAGCTCGGGCTGTCTGTGGCTTCTCCAGCCGCGGGCGCGCGCCAGTCCCACT | 324 |
| Db | 181 | ACCGAGCTCGGGCTGTCTGTGGCTTCTCCAGCGCGGGCGCGCGCCAGTCCCACT | 240 |
| Qy | 325 | TCCTCCTATACCTCTCCCAAAACAAGCCCAAGGCGCGAGGGGTGGACAACCCAGCGGT | 384 |
| Db | 241 | TCCTCCTATACCTCTCCCAAAACAAGCCCAAGGCGCGAGGGGTGGACAACCCAGCGGT | 300 |
| Qy | 385 | TCTCGGCAAGAGTGTGGGGACACTTCGTCTCTCACCTGAGCGACTTCGCGCGAGAGA | 444 |
| Db | 301 | TCTCGGCAAGAGTGTGGGGACACTTCGTCTCTCACCTGAGCGACTTCGCGCGAGAGA | 360 |
| Qy | 445 | ACGAGGGCTACTATTCTCTCGGCCCTGAGCAACTCCATCATGTACTTCAGCCACTTCG | 504 |
| Db | 361 | ACGAGGGCTACTATTCTCTCGGCCCTGAGCAACTCCATCATGTACTTCAGCCACTTCG | 420 |
| Qy | 505 | TGCGGCTCTCTGCGAGGAGCCACAACAGCCGACGCGCGGACACCAACACCGG | 564 |
| Db | 421 | TGCGGCTCTCTGCGAGGAGCCACAACAGCCGACGCGCGGACACCAACACCGG | 480 |
| Qy | 565 | CGCCACCATCGCTCGAGCCCTGTCTCTCGGCCAGAGCGCTGCCGGCAGCGCGG | 624 |
| Db | 481 | CGCCACCATCGCTCGAGCCCTGTCTCTCGGCCAGAGCGCTGCCGGCAGCGCGG | 540 |

QY 181 CGAGCCAGTTCCGGGTGTCGGCGCTGGATCGGACCTGGAACTTGGCGGAGACAGTGGAGC 240
Db 181 CGAGCCAGTTCCGGGTGTCGGCGCTGGATCGGACCTGGAACTTGGCGGAGACAGTGGAGC 240
QY 241 TGAAGTGCAGGTGCTGCTGCTCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
Db 241 TGAAGTGCAGGTGCTGCTGCTCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCGCG 300
QY 301 CGCGCGCCGCCAGTCCCACTTCTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
Db 301 CGCGCGCCGCCAGTCCCACTTCTCTCTATACCTCTCCCAAAAGCCCAAGGCGG 360
QY 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCTGCTCA 420
Db 361 CGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTCTGCTCA 420
QY 421 CCTTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAACT 480
Db 421 CCTTGAGCGACTTCCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAACT 480
QY 481 CCATCATGTACTTCAGCCACTTCTGCGCGTCTTCTGCGAGCGAAGCCACCGACGC 540
Db 481 CCATCATGTACTTCAGCCACTTCTGCGCGTCTTCTGCGAGCGAAGCCACCGACGC 540
QY 541 CAGCGCCGCGACCAACACCGCGGCCCAACCATCGCTCGAGGCCCTGCTCGGCC 600
Db 541 CAGCGCCGCGACCAACACCGCGGCCCAACCATCGCTCGAGGCCCTGCTCGGCC 600
QY 601 CAGAGCGTGGCGGCGGCGGCGGCGAGTGCACACGAGGGGGCTGACCTTCGCT 660
Db 601 CAGAGCGTGGCGGCGGCGGCGGCGGCGAGTGCACACGAGGGGGCTGACCTTCGCT 660
QY 661 GTGATATCTACATCTGGGCGGCTTGGCGGCGGCTTGTGGGCTCTTCTGCTCACTGG 720
Db 661 GTGATATCTACATCTGGGCGGCTTGGCGGCGGCTTGTGGGCTCTTCTGCTCACTGG 720
QY 721 TTATCACCCTTTACTGCAACCAACGAGAACCGAGACGTTGTTGCAAAATGTCGCGGCTG 780
Db 721 TTATCACCCTTTACTGCAACCAACGAGAACCGAGACGTTGTTGCAAAATGTCGCGGCTG 780
QY 781 TGGTCAAAATCGGAGACAAAGCCAGCTTTGGCGGAGATACGCTTAAACCTGTGCAACAG 840
Db 781 TGGTCAAAATCGGAGACAAAGCCAGCTTTGGCGGAGATACGCTTAAACCTGTGCAACAG 840
QY 841 CCATCATATTAATCAAACTGAGATCTTCTCTTTTGGGAGCAAGTCTTCCCTTCAT 900
Db 841 CCATCATATTAATCAAACTGAGATCTTCTCTTTTGGGAGCAAGTCTTCCCTTCAT 900
QY 901 TTTTTCAGTCTTCTCCTGTGATTCATCTCATGATTAATTTAGTGGGGCGGG 960
Db 901 TTTTTCAGTCTTCTCCTGTGATTCATCTCATGATTAATTTAGTGGGGCGGG 960
QY 961 GTGGGAAAGATTACTTTTCTTATGTTTGAACGGGAAACAAACTAGGTAAATCTAC 1020
Db 961 GTGGGAAAGATTACTTTTCTTATGTTTGAACGGGAAACAAACTAGGTAAATCTAC 1020
QY 1021 AGTACACCAAGGGTCACACTACTGTTGTGCGCACATCGCGGTAGGGCTGGAAGGGG 1080
Db 1021 AGTACACCAAGGGTCACACTACTGTTGTGCGCACATCGCGGTAGGGCTGGAAGGGG 1080
QY 1081 CAGGCGAGAGTACCGCGAGGTTCTCAGAAATCATGCTGAGAGCTGGAGGCCCATG 1140
Db 1081 CAGGCGAGAGTACCGCGAGGTTCTCAGAAATCATGCTGAGAGCTGGAGGCCCATG 1140
QY 1141 CCATCTCAACCTTCTCCCGCCGTTTACAAAGGGGAGGCTAAAGCCGAGACAGCT 1200
Db 1141 CCATCTCAACCTTCTCCCGCCGTTTACAAAGGGGAGGCTAAAGCCGAGACAGCT 1200
QY 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTACTGAGGAGCTTGTCTCCA 1260
Db 1201 TGATCAAGGCGACACAGCAAGTCAAGGTTGGAGCAGTACTGAGGAGCTTGTCTCCA 1260
QY 1261 GCTCAGGGCTCTTCTCTCCACACCATTCAGGTTCTTCTTCCGAGGCCCTGCTCAGGG 1320

Db 1261 GCTCAGGGCTCTTCTCTCCACCATTCAGGTTCTTCTTCCGAGGCCCTGCTCAGGG 1320
QY 1321 TGAGGTGCTTGGTCTCCACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATACTGT 1380
Db 1321 TGAGGTGCTTGGTCTCCACGCGCAAGGAAACAAGTACTTCTTGATACCTGGGATACTGT 1380
QY 1381 GCCCAGAGCTCGAGGAGGTAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
Db 1381 GCCCAGAGCTCGAGGAGGTAATGAATTAAGAGAGAGAACTGCCTTTGGCAGAGTTCTAT 1440
QY 1441 AATGTAAACAATATCAGACTTTTTTTTTTATATCAAGCCCTAAATTTGATAGACCTAA 1500
Db 1441 AATGTAAACAATATCAGACTTTTTTTTTTATATCAAGCCCTAAATTTGATAGACCTAA 1500
QY 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
Db 1501 AATAAAATGAAGTGGTGAAGCTTAAACCTCGGAAATGAATCCCTCTATCTCTAAAGAAAT 1560
QY 1561 CTCTGTGAAACCCCTATGTGGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCGAGAGGG 1620
Db 1561 CTCTGTGAAACCCCTATGTGGAGGCGGAATTTGCTCTCCAGCCCTTGCAATTCGAGAGGG 1620
QY 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
Db 1621 CCCATGAAGAGGACAGGCTACCCCTTTACAAATAGAAATTTGAGCATCAGTGAGGTTAAA 1680
QY 1681 CTAAGGCGCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCAGTGATGA 1740
Db 1681 CTAAGGCGCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCAGTGATGA 1740
QY 1741 CTTTATTATCTTGTAAAGACAAATTTGGAGAGGCCCTCACAAGCCCTGSCCTCTGCT 1800
Db 1741 CTTTATTATCTTGTAAAGACAAATTTGGAGAGGCCCTCACAAGCCCTGSCCTCTGCT 1800
QY 1801 CAATAGCAGATACAGGATCAGGACAGCTGACCTCTCTTAAAGGAGGCTGAGAGCCCAA 1860
Db 1801 CAATAGCAGATACAGGATCAGGAGACAGCTGACCTCTCTTAAAGGAGGCTGAGAGCCCAA 1860
QY 1861 CTGCTGTCCCAACATGCACTTCTTCTTAAAGGTATGTTACAGCAATGCTGCCCAAT 1920
Db 1861 CTGCTGTCCCAACATGCACTTCTTCTTAAAGGTATGTTACAGCAATGCTGCCCAAT 1920
QY 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTTCACTTAG 1980
Db 1921 GGAGAGAAAACTTAAGTAGATAAGGAAATAAGAACCACTCATTAATTTCTTCACTTAG 1980
QY 1981 AATAATCTCTGTTAATATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
Db 1981 AATAATCTCTGTTAATATGTTGATACATTTCTTCTGATTTATTTCTACACATACATGTA 2040
QY 2041 AATATGCTTCTTTTAAATAGGTTGTTACTATGCTTATGAGTGGCTTTAATGAAT 2100
Db 2041 AATATGCTTCTTTTAAATAGGTTGTTACTATGCTTATGAGTGGCTTTAATGAAT 2100
QY 2101 AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2160
Db 2101 AAACATTTGTAGCATCTCTTTAATGGTAAACAGCAAAAAAAGGAGGAGGAGGAGGAGG 2160
QY 2161 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
Db 2161 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2220
QY 2221 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2281
Db 2221 AAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2281

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/ APPLICANT: Ludwig Institute for Cancer Research et al.
/ TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
/ FILE REFERENCE: 28967/39178
/ CURRENT APPLICATION NUMBER: US/10/505,928
/ CURRENT FILING DATE: 2004-08-27
/ PRIOR APPLICATION NUMBER: US 60/363,019
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: PatentIn 3.2
/ SEQ ID NO 758
/ LENGTH: 1999
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-505-928-758

Query Match          6.0%; Score 134.6; DB 6; Length 1999;
Best Local Similarity 70.8%; Pred. No. 4.2e-11;
Matches 179; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 2009 TCTTCTGATATTTCTACACATACATGTAATAATATGCTTTCTTTTAAATAGGGTT 2068
Dbb 1724 TTTTGTAGAGAAATTAGAACCCATACACAGGCTATCAACATGTTATTCAATGG 1783
QY 2069 GTACTATGCTGTATGAGTGGCTTTAATCAATAAACAATTTGACATCTCTTTAATGG 2128
Dbb 1784 ACACCTAACTCTTTTCTATTGTTTTTAAGTAAGACTTTTATTAAATAAACAATAATG 1843
QY 2129 TAAACAGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2188
Dbb 1844 TTTGAGCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1903
QY 2189 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2248
Dbb 1904 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1963
QY 2249 AAAAAAATAAAAAA 2261
Dbb 1964 AAAAAAATAAAAAA 1976

RESULT 3
US-10-953-349-37996
/ Sequence 37996, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37996
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Zea mays subsp. mays
US-10-953-349-37996

Query Match          5.8%; Score 131; DB 6; Length 2040;
Best Local Similarity 87.7%; Pred. No. 1.3e-10;
Matches 143; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2099 ATAAACATTGTGACATCTCTTTAATGGTTAAACAGCAAAAAAATAAAAAAATAAAAAA 2158
Dbb 1730 AGATAAGTTTGTAGTTGATTATATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1789
QY 2159 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2218
Dbb 1790 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 1849
QY 2219 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2261
Dbb 1964 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
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Db 1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1892

RESULT 4
US-11-145-307A-29
/ Sequence 29, Application US/11145307A
/ Publication No. US20060094035A1
/ GENERAL INFORMATION:
/ APPLICANT: Arcturus Bioscience, Inc.
/ APPLICANT: Brlander, Mark G.
/ APPLICANT: Ma, Xiao-Jun
/ TITLE OF INVENTION: Identification of Tumors
/ FILE REFERENCE: 022041-002020US
/ CURRENT APPLICATION NUMBER: US/11/145,307A
/ CURRENT FILING DATE: 2005-06-03
/ PRIOR APPLICATION NUMBER: US 60/577,084
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 268
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29
/ LENGTH: 4670
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-145-307A-29

Query Match          5.8%; Score 130.6; DB 7; Length 4670;
Best Local Similarity 83.6%; Pred. No. 1.5e-10;
Matches 148; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 2076 GCTGTATGAGTGGCTTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGTAAACAG 2135
Dbb 4494 GCTTTTTTGTGGGTTTTTATTTTAAAGAAACACTCAATCATCTCTTAAAAAATAAAAA 4553
QY 2136 CAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2195
Dbb 4554 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4613
QY 2196 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 2252
Dbb 4614 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4670

RESULT 5
US-10-196-749-169
/ Sequence 169, Application US/10196749
/ Publication No. US20060094864A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C340
/ CURRENT APPLICATION NUMBER: US/10/196,749
/ CURRENT FILING DATE: 2002-07-16
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
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; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 169
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-169

Query Match 5.7%; Score 129.4; DB 6; Length 2846;
Best Local Similarity 84.8%; Pred. No. 2.1e-10;
Matches 145; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2091 TTTAATGAATAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2150
Db 2668 TCTCTGTACACATTTAATAAATAAGGGTTGGCTTCTGAACCTACAAAAA 2727

Qy 2151 AAAAAA 2210
Db 2728 AAAAAA 2787

Qy 2211 AAAAAA 2261
Db 2788 AAAAAA 2838

RESULT 6
US-11-101-316-37
; Sequence 37, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Auscin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/066867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 37
; LENGTH: 2846
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-37

Query Match 5.7%; Score 129.4; DB 7; Length 2846;
Best Local Similarity 84.8%; Pred. No. 2.1e-10;
Matches 145; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 2091 TTTAATGAATAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2150
Db 2668 TCTCTGTACACATTTAATAAATAAGGGTTGGCTTCTGAACCTACAAAAA 2727

Qy 2151 AAAAAA 2210
Db 2728 AAAAAA 2787

Qy 2211 AAAAAA 2261
Db 2788 AAAAAA 2838

RESULT 7
US-10-953-349-35802
; Sequence 35802, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35802
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (539)..(539)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (659)..(660)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2409)..(2411)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2432)..(2433)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-35802

Query Match 5.7%; Score 128.4; DB 6; Length 2442;
Best Local Similarity 87.0%; Pred. No. 2.9e-10;
Matches 141; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 2100 TAAACATTTGTAGCATCCTCTTTAATGGTAAACAGCAAAAAA 2159
Db 2211 TACATACCCGAAGGTTGCTCTTGACATAAAAA 2270

Qy 2160 AAAAAA 2219
Db 2271 AAAAAA 2330

Qy 2220 AAAAAA 2261
Db 2331 AAAAAA 2372

RESULT 8
US-10-196-749-27
; Sequence 27, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc

```
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 27
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-27

Query Match          5.6%; Score 126; DB 6; Length 1985;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2136 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2195
Db 1858 CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1917
QY 2196 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2255
Db 1918 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1977
QY 2256 AAAAAA 2261
Db 1978 AAAAAA 1983

RESULT 9
US-10-196-749-149
; Sequence 149, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
```

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; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 149
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-149

Query Match          5.6%; Score 126; DB 6; Length 2773;
Best Local Similarity 93.0%; Pred. No. 6.1e-10;
Matches 132; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2120 TTTAATGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2179
Db 2631 TTAATGTTTAGAGATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2690
QY 2180 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2239
Db 2691 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2750
QY 2240 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db 2751 AAAAAAAAAAAAAAAAAAAAAA 2772

RESULT 10
US-11-101-316-33
; Sequence 33, Application US/11101316
; Publication No. US2006009657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/06867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
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; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 33
; LENGTH: 2773
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-33

Query Match          5.6%; Score 126; DB 7; Length 2773;
Best Local Similarity 93.0%; Pred. No. 6.1e-10;
Matches 132; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy  2120 TTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2179
Db  2631 TTTAATGTTAGAGGATGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2690

Qy  2180 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2239
Db  2691 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2750

Qy  2240 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db  2751 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2772

RESULT 11
US-10-953-349-37381
; Sequence 37381, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37381
; LENGTH: 2272
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; NAME/KEY: misc feature
; LOCATION: (2086)..(2086)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-37381

Query Match          5.4%; Score 121.6; DB 6; Length 2272;
Best Local Similarity 80.2%; Pred. No. 2.4e-09;
Matches 142; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy  2085 AGTGCTTTAATGAATAAACATTTGTAGCATCTCTTTAATGGGTAAACAGCAAAAAA 2144
Db  2019 ACTGAGTTACAGCAGCAATGAATTTCTCGATCCTAAATGCAGAGAAATAAATAAATAA 2078

Qy  2145 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2204
Db  2079 TATATAAAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2138

Qy  2205 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2261
Db  2139 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2195

RESULT 12
US-10-953-349-7328
; Sequence 7328, Application US/10953349
; Publication No. US20060107345A1
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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7328
; LENGTH: 2861
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7328

Query Match          5.2%; Score 117.8; DB 6; Length 2861;
Best Local Similarity 66.1%; Pred. No. 7.9e-09;
Matches 170; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

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Db  1502 TTTGGCTCCCTTGTGGATGATGTTGGTATATGATGATGATATACACAGAGGCTCTATG 1561

Qy  2057 TTTAATAGGGTTGACTATCTGCTTATCAGTGGCTTTAATGAATAAACATTTGTAGCATC 2116
Db  1562 TAAATAACGTTTCTCGTTTTTTTATCCTGTAATCATCTTATTTTCTTTTAAACATG 1621

Qy  2117 CTCTTTAATGGGTAAACAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2176
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Qy  2177 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2236
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RESULT 13
US-10-953-349-37514
; Sequence 37514, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37514
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37514

Query Match          5.2%; Score 116.8; DB 6; Length 2163;
Best Local Similarity 88.2%; Pred. No. 1.1e-08;
Matches 127; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy  2170 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2229
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Qy  2230 AAAAAAAAAAAAAAAAAAAAAA 2253
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GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 30, 2006, 03:27:54 ; Search time 9648 Seconds
(without alignments)
13104.644 Million cell updates/sec

Title: US-10-804-763-2
Perfect score: 2261
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

CR619549 1948 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI070YG17 of Placenta Cot 25-normalized
of Homo sapiens (human).
CR619549
CR619549.1 GI:50500356
HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1948)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1948)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 94.6%; Pred. No. 0; Matches 1948; Conservative 0; Mismatches 0; Indels 111; Gaps 1;

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VERSION    AL575755.3  GI:46248682
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REFERENCE  1 (bases 1 to 936)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On Feb 16, 2001 this sequence version replaced gi:31314055.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
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            For more information about this cluster, see
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Best Local Similarity 97.1%; Pred. No. 2e-157;
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VERSION    BX415858.2  GI:46955857
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ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE  1 (bases 1 to 918)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished (2001)
COMMENT   On May 15, 2003 this sequence version replaced gi:30767592.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
            was not normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
            This sequence belongs to sequence cluster 1670.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0CAP008B1NP1&c=1670.r.

FEATURES             Location/Qualifiers
     source           1..918
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"

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| Db | 241 | CGGCGCGCGCGCGCAGTCCACCTTCTCTCTATACCTCTCCAAACACAGCCCAAGCGCGC | 300 |
| Qy | 362 | CGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTAC | 421 |
| Db | 301 | CGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTAC | 360 |
| Qy | 422 | CTGAGCGCATCTTCGGCGGAGAGAAAGAGGGCTACTATTTCTCTCGGCGCTGAGCAATC | 481 |
| Db | 361 | CTGAGCGCATCTTCGGCGGAGAGAAAGAGGGCTACTATTTCTCTCGGCGCTGAGCAATC | 420 |
| Qy | 482 | CATCATGTACTTCAGCACTTCGTGCGGCTCTTCCTGCCAGCGAGCCACACAGCGC | 541 |
| Db | 421 | CATCATGTACTTCAGCACTTCGTGCGGCTCTTCCTGCCAGCGAGCCACACAGCGC | 480 |
| Qy | 542 | AGCGCGCGACCAACCAACCGCGGCCACCATCGGTCCAGCGCCCTGTCTCTCGGCC | 601 |
| Db | 481 | AGCGCGCGACCAACCAACCGCGGCCACCATCGGTCCAGCGCCCTGTCTCTCGGCC | 540 |
| Qy | 602 | AGAGGCGTCCGGCCAGCGCGGGGGCGCAGTGACACAGAGGGGCTGGACTTCGCCCTG | 661 |
| Db | 541 | AGAGGCGTCCGGCCAGCGCGGGGGCGCAGTGACACAGAGGGGCTGGACTTCGCCCTG | 600 |
| Qy | 662 | TGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTAC-TGG | 720 |
| Db | 601 | TGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTAC-TGG | 660 |
| Qy | 721 | TTATCACCTTTACTGCAACACAGAAACCGAAGACGTGTTTGCAAAATGTCGCCGCGCTG | 780 |
| Db | 661 | TTATCACCTTTACTGCAACACAGAAACCGAAGACGTGTTTGCAAAATGTCGCCGCGCTG | 720 |
| Qy | 781 | TGGTCAAAATCGGG--AGACAAGCCAGCGCTTTCGGCGAGATACGTCTAAACC--TGTGCA | 836 |
| Db | 721 | TGGTCAAAATCGGGGAGACATGCCAGCTTTTCGGGAGATACGTCTAAACCCTGTGCA | 780 |
| Qy | 837 | ACAGCCATPAC-ATTACTTCAAACCTGAGATCCTTCTTTTGAGGAGCAAGTCTTCCT | 895 |
| Db | 781 | TCAGCCACTACAATTACTTCAAACCTGAGATCCTTCTTATAGAGGAGCAAGTCTTCCT | 840 |
| Qy | 896 | TTCAATTTTTCAGTCTTCTCTCTCTGTGATTCATCTCAT | 936 |
| Db | 841 | TTCAATATTATACAGGCTCTCTCTCTGTGTATTTCATCAT | 881 |
| RESULT 5 | | | |
| LOCUS | BI819839 | | |
| DEFINITION | 603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5', mRNA sequence. | 789 bp | linear EST 04-OCT-2001 |
| ACCESSION | BI819839 | | |
| VERSION | BI819839.1 | GI:15931389 | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | | |
| REFERENCE | 1 (bases 1 to 789) | | |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/ . | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| JOURNAL | Unpublished (1999) | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11454 row: d column: 18 | | |


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Qy 764 CAATGTCCCGGCTGTGGTCAATCGGGAGACAAGCCCGCCTTTTCGGCGAGATACGT 823
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Qy 824 CTAACCCCTG 832
Db 781 CTAACCCCTG 789

RESULT 6
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LOCUS DA931234 SPLEN1 Homo sapiens cDNA clone SPLEN1000141 5', mRNA
DEFINITION DA931234 sequence.
ACCESSION DA931234
VERSION DA931234.1 GI:82056788
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Kimura K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakeguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
TITLE Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES             Location/Qualifiers
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ORIGIN
Query Match      33.8%; Score 764.8; DB 9; Length 838;
Best Local Similarity 99.4%; Pred. No. 4e-135;
Matches 777; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 32 AACTTTCCCTCGCGCCCGCCACCGGCTCCCGCGCGCTCCCTCGCGCCGAGCTTCG 91
Db 1 AACTTTCCCTCGCGCCCGCCACCGGCTCCCGCGCGCTCCCTCGCGCCGAGCTTCG 60

Qy 92 ACCCAGCAGCTCTCGGGAGCGGTCTATGCGCTTACAGTACGCGCTTCCTCGCC 151
Db 61 AGCCAGCAGCGTCTCGGGAGCGGTCTATGCGCTTACAGTACGCGCTTCCTCGCC 120

Qy 152 GCTGGCCTTGCTGCTCCAGCGCCGAGGCGGAGCAGTCCCGGCTGTCGCGCTGGATCG 211
Db 121 GCTGGCCTTGCTGCTCCAGCGCCGAGGCGGAGCAGTTCGCGGCTGTCGCGCTGGATCG 180

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Qy 212 GACCTGAACTCTGGCGAGACAGTGGAGCTGAAAGTGCAGAGTGTCTGTCTCAACCCGAC 271
Db 181 GACCTGAACTCTGGCGAGACAGTGGAGCTGAAAGTGCAGAGTGTCTGTCTCAACCCGAC 240

Qy 272 GTGGGCTGCTGCTGGGCTCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCTCTCT 331
Db 241 GTGGGCTGCTGCTGGGCTCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCTTCTCTCT 300

Qy 332 ATACCTCTCCCAAAACAAAGCCCAAGGCGCGCGAGGGCTGGACACCCAGCGGTTCTCGGG 391
Db 301 ATACCTCTCCCAAAACAAAGCCCAAGGCGCGCGAGGGCTGGACACCCAGCGGTTCTCGGG 360

Qy 392 CAAGAGGTTGGGGACACCTTCTCTCACCTCAGCGACTTCCGCCGAGAGAACGAGGG 451
Db 361 CAAGAGGTTGGGGACACCTTCTCTCACCTCAGCGACTTCCGCCGAGAGAACGAGGG 420

Qy 452 CTACTATTCTGCTCGGCCCTGAGCACTCATCATGTACTTTCAGCCACTTTCGTGCCCGT 511
Db 421 CTACTATTCTGCTCGGCCCTGAGCACTCATCATGTACTTTCAGCCACTTTCGTGCCCGT 480

Qy 512 CTTCTCTGCAGCGAAGCCCAACACGAGCGCCGCGCGAGCCCAACACCGCGGCCAC 571
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Qy 572 CATCGCTCGAGCGCCCTTCTCTCGCCGAGAGCGGTGCCGCCGAGAGAGCGGGGGCGC 631
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Qy 632 AGTCACACGAGGGGCTTGGACTTTCGCTGTGATATCTACATCTGGGCGCCCTTCGCGCG 691
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Qy 692 GACTTGTGGGTCCTTCTCTGTCTCAGTGGTATCACCCCTTACTCAACACGAGAACCG 751
Db 661 GACTTGTGGGTCCTTCTCTGTCTCAGTGGTATCACCCCTTACTCAACACGAGAACCG 720

Qy 752 AAGACGTTTGGCAATGTCCCGGCTTGGTCAATCGGGAGACAGCCAGCTTTC 811
Db 721 AAGACGTTTGGCAATGT-CCCGGCTTGGTCAATCGGGAGACAGCCAGCTTTC 779

Qy 812 GG 813
Db 780 GG 781

RESULT 7
BX437211/c
LOCUS BX437211 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP005YB16
DEFINITION 3-PRIME, mRNA sequence.
ACCESSION BX437211
VERSION BX437211.2 GI:47009751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 847)
AUTHORS Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30781554.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

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This sequence belongs to sequence cluster 1670.1
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CSOCAP005DA08NP1&c=1670.1.r>.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP005YB16"
/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/notes="Vector: pCMVSPORT6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 33.8%; Score 763.4; DB 4; Length 847;
Best Local Similarity 91.9%; Pred. No. 7.4e-135;
Matches 779; Conservative 47; Mismatches 19; Indels 3; Gaps 3;
QY 1263 TCAGGGCTCTTCCCTCCACACCATTCAGGCTCTTCTTCGAGGCCCTGTCTCAGGGTG 1322
DB 847 TCAGGKTCTTTCCCCACACATTCGTTTCTTTTCGAGGCCCTTTTCAGGGTG 788
QY 1323 AGGTGCTTGAGTCTCAACGGCAAGGAACTCTTCTGATACCTGGGATCTGTGC 1382
DB 787 AGKTGTTTATYNCACACGGCAAGGNAAYAKTWTCTTGTATCTACGATCTGKGC 728
QY 1383 CCAGAGCTCGAGGAGTGAATGAAT-AAAGAGAGAACTGCTTTGGCAGAGTTCTATA 1441
DB 727 CCAGAGCTCGAGGAGTGAATGAATTAAGAGAGAACTGCTTTGGCAGAGTTCTATA 668
QY 1442 ATGTAAACATATCAGCTTTTCTTTTATATCAAGCTTAAATTTGTATAGCTTAA 1501
DB 667 WTGTAAACATWTCTAKWTCTTTTATATCAAGCTTAAATTTGTATAGCTTAA 608
QY 1502 ATAAATGAAGTGGTGAAGCTTAACCTGGAAATGAATCCCTCTATCTCTAAAGAAATC 1561
DB 607 WTAAATGAAGTGGTGAAGCTTAACCTGGAAATGAATCCCTCTTWTCTTAAAGAAAT 548
QY 1562 TCTGTGAACCCCTATGTGGAGCGGAATGTCTCCAGCCCTGTGATTCAGAGGGGC 1621
DB 547 TTT-TGAACCCCTTGTGTGGAGCGGAATGTCTCCAGCCCTGTGATTCAGAGGGGC 489
QY 1622 CCATGAAGAGACAGGCTACCCCTTTACAATAGAAATTTGAGCATCAGTGAAGTTAAC 1681
DB 488 CCATGAAGAGACAGGCTACCCCTTTACAATAGAAATTTGAGCATCAGTGAAGTTAAC 429
QY 1682 TAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCACTGATGAC 1741
DB 428 TAAGGCCCTCTTGAATCTCTGAATTTGAGATACAAACATGTTCTCGGATCACTGATGAY 369
QY 1742 TTTTATATCTTTGTAAGACAATTTGTGGAGAGCCCTCACACAGCCCTTGCTCTGTCTC 1801
DB 368 TTTTATATCTTTGTAAGACAATTTGTGGAGAGCCCTCAVACAGCCCTTGCTCTGTCTC 309
QY 1802 TACTAGCATACAGGATGAGGACACCTGACTCTCTTAAGAGGCTGAGAGCCCAAC 1861
DB 308 AATAGCATACAGGATGAGGACACCTGACTCTCTTAAGAGGCTGAGAGCCCAAC 249
QY 1862 TGCTGTCCCAACATGCACCTCTCTTGAAGTATGGTATGAGCAATGCTTCCCTGATG 1921
DB 248 TGCTGTCCCAACATGCACCTCTCTTGAAGTATGGTATGAGCAATGCTTCCCTGATG 189
QY 1922 GAGAGAAAAAATTAAAGTATAGATAAGAAATAAGAACCACTATAATTTCTACCTTAGGA 1981
DB 188 GAGAGAAAAAATTAAAGTATAGATAAGAAATAAGAACCACTATAATTTCTACCTTAGGA 129
QY 1982 ATAATCTCTGTATATGGTGTACATCTTCTGATATTTTCTACATACATGATAA 2041
DB 128 ATAATCTCTGTATATGGTGTACATCTTCTGATATTTTCTACATACATGATAA 69

QY 2042 ATATGTCTTTCTTTTAAATAGGTTGTACTATGCTGTTA-TGAGTGGCTTTAATGAAT 2100
DB 68 ATATGTCTTTCTTTTAAATAGGTTGTACTATGCTGTTA-TGAGTGGCTTTAATGAAT 9
QY 2101 AAACATTT 2108
DB 8 AWAYTTT 1

RESULT 8

BI820808
LOCUS 603034019F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
DEFINITION mRNA sequence.
ACCESSION BI820808
VERSION BI820808.1 GI:15932358
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11436 row: e column: 06
High quality sequence stop: 802.

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5175149"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 Kb, insert size range 1-3 Kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 32.9%; Score 744.8; DB 2; Length 804;
Best Local Similarity 98.1%; Pred. No. 2.6e-131;
Matches 785; Conservative 0; Mismatches 12; Indels 3; Gaps 3;
QY 123 GCCTTACCAGTGACCGCTTGCTCTCGCGCTGGCTTGCTCTCCAGCCGCGAGCGG 182
DB 4 GCTTACCAGTGACCGCTTGCTCTCGCGCTGGCTTGCTCTCCAGCCGCGAGCGG 63
QY 183 AGCCAGTTCCCGGTTGCGCGCTGGATCGGACCTCGGACCTGGCGGAGACAGTGGAGCTG 242
DB 64 AGCCAGTTCCCGGTTGCGCGCTGGATCGGACCTGGCGGAGACAGTGGAGCTG 123
QY 243 AAGTCCAGGTTGCTGCTGTCCAAACCGAGCTGGGCTGCTGTGGCTCTTCCAGCGCGC 302
DB 124 AAGTCCAGGTTGCTGCTGTCCAAACCGAGCTGGGCTGCTGTGGCTCTTCCAGCGCGC 183

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QY 303 GCGCGCGCGCGAGTCCACCTTCTCTCTATACCTTCCCAAAACAAGCCCAAGCGCGCC 362
Db 184 GCGCGCGCGCGAGTCCACCTTCTCTCTATACCTTCCCAAAACAAGCCCAAGCGCGCC 243
QY 363 GAGGGCTGGACACCCACCGGTTCTCGGGCAAGAGTTGGGGACACCTTCTCTCTACC 422
Db 244 GAGGGCTGGACACCCACCGGTTCTCGGGCAAGAGTTGGGGACACCTTCTCTCTACC 303
QY 423 CTGAGCGCACTTCCGCGGAGAGAAAGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACTCC 482
Db 304 CTGAGCGCACTTCCGCGGAGAGAAAGAGGGCTACTATTTCTGCTCGGCCCTGAGCAACTCC 363
QY 483 ATCATGTACTTACGACACTTGTGCGCGTCTTCTGCGAGGAGCCACCAAGCGCA 542
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QY 543 GCGCGCGCACCAACACCGCGCCACCATCGGTCGACGCCCTGTCTCGGCCCA 602
Db 424 GCGCGCGCACCAACACCGCGCCACCATCGGTCGACGCCCTGTCTCGGCCCA 483
QY 603 GAGCGGTCCGCGCGCGCGGGCGCGAGTGACACAGAGGGGCTGGACTTGCCTGT 662
Db 484 GAGCGGTCCGCGCGCGCGGGCGCGAGTGACACAGAGGGGCTGGACTTGCCTGT 543
QY 663 GATATCTACATCTGGGCGGCTTGGCGGGAGTGTGGGGTCTTCTCTCTGCTACTGTT 722
Db 544 GATATCTACATCTGGGCGGCTTGGCGGGAGTGTGGGGTCTTCTCTCTGCTACTGTT 603
QY 723 ATCACTCTTACTGCAACACAGGAACGAGAGCTGTTGCAATGTCCTCGGCTGT 782
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QY 783 GTCAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCT-AAACCTGTGCAACAGC 841
Db 664 GTCAATCGGAGACAAGCCAGCCCTTTCGGCGAGATACGTCTAAACCTGTGCAACAGC 723
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Db 724 CACTACATTACTTTCAAATCTGAGATCTTCTTTTGGAGGAGCAAGTCTTCCCTTTTCA 783
QY 901 TTTTTC-CCAGTCTTCTCC 919
Db 784 TTTTTCAGTCTTCTCTCC 803

RESULT 9
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LOCUS 603043151F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
DEFINITION mRNA sequence.
ACCESSION BI760947
VERSION BI760947.1 GI:15752525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: e column: 13
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High quality sequence start: 4
High quality sequence stop: 756.
Location/Qualifiers
1. 780

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183604"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colonies, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 32.0%; Score 724.4; DB 2; Length 780;
Best Local Similarity 98.7%; Pred. No. 2e-127;
Matches 762; Conservative 0; Mismatches 6; Indels 4; Gaps 3;

QY 54 ACCGGCTCCCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAAAGCAGCTCTGGGAG 113
Db 1 ACCGGCTCCCGCGCGCTCCCTCGCGCCCGAGCTTCGAGCCAAAGCAGCTCTGGGAG 60
QY 114 CGGCTCATGGCTTACAGTGACCGCTTGTCTCTCGCGCTGGCTTGTCTCTCACGCC 173
Db 61 CGGCTCATGGCTTACAGTGACCGCTTGTCTCTCGCGCTGGCTTGTCTCTCACGCC 120
QY 174 GCCAGCGCGAGCTTCGGGCTGTGGCGCTGGATCGGACTGTGAACTTGGGCGAGACA 233
Db 121 GCCAGCGCGAGCTTCGGGCTGTGGCGCTGGATCGGACTGTGAACTTGGGCGAGACA 180
QY 234 GTGAGCTGAAGTGCAGGCTGTCTGTCTCAACCGGAGCTCGGGCTGTCTGTGCTCTTC 293
Db 181 GTGAGCTGAAGTGCAGGCTGTCTGTCTCAACCGGAGCTCGGGCTGTCTGTGCTCTTC 240
QY 294 CAGCGCGCGCGCGCGCGCGCGCGAGTCCCACTTCTCTATACCTTCTCCAAACAGGCC 353
Db 241 CAGCGCGCGCGCGCGCGCGCGCGAGTCCCACTTCTCTATACCTTCTCCAAACAGGCC 300
QY 354 AAGCGCGCGAGGGCTGGACACCGCGGTTCTCGGGCAAGAGTTCGGGGACACCTTC 413
Db 301 AAGCGCGCGAGGGCTGGACACCGCGGTTCTCGGGCAAGAGTTCGGGGACACCTTC 360
QY 414 GTCCTCACCTTACGAGCTTCCGCGGAGAGAAAGAGGCTACTATTTCTGTCTGGCCCTG 473
Db 361 GTCCTCACCTTACGAGCTTCCGCGGAGAGAAAGAGGCTACTATTTCTGTCTGGCCCTG 420
QY 474 AGCAACTCATATGTAATTCAGCCACTTGTGCGGCTTCTCTCTCCAGCGAGGCCACC 533
Db 421 AGCAACTCATATGTAATTCAGCCACTTGTGCGGCTTCTCTCTCCAGCGAGGCCACC 480
QY 534 ACGCGCGCAGCG 593
Db 481 ACGCGCGCAGCG 540
QY 594 CTGCGCCAGAGGGCTGCG 653
Db 541 CTGCGCCAGAGGGCTGCG 600
QY 654 TTGCGCTGTATATCTACATCTGGCGCGCTTGGCGGGAGCTTGTGGGCTCTCTCCG 713
Db 601 TTGCGCTGTATATCTACATCTGGCGCGCTTGGCGGGAGCTTGTGGGCTCTCTCCG 660
QY 714 TCACTT--GGTTATCACCCCTTTTACTGCAACCAACGAGAACCGAGAGCTGTTTCAATGTC 771
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Db 661 TCACCTGGTATACACCCCTTACTGCAACACACAGAACCGAGACGCTGTTTGC-AATGTC 719

QY 772 CCGGCGCTGTGGTCAAAATCGGAGACAGCCAGCC-TTTTCGGCGAGATACG 822

Db 720 CCGGCGCTGTGGTCAAAATCGGAGACAGCCAGCCCTTTTCGGCGAGATACG 771

RESULT 10
 AW949684 749 bp mRNA linear EST 01-JUN-2000
 LOCUS EST361754 MAGE resequenes, MAGA Homo sapiens cDNA, mRNA sequence.
 DEFINITION AW949684
 ACCESSION AW949684.1 GI:8139317
 VERSION
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
 Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
 Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 5

Seq primer: Reverse.

Location/Qualifiers

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FEATURES
 source

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 Best Local Similarity 98.5%; Pred. No. 2.6e-124;
 Matches 725; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

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 Db 1 ACAAACCTAGGTAAATCTACAGTACACCAAGGTCACATCTGTTGGGCACATC 60

QY 1060 GCGGTAGGCGTGGAAAGGGCGAGGTCAGCTACCGCAGAGTCTTCAGATCATGCTG 1119

Db 61 GCGGTAGGCGTGGAAAGGGCGAGGTCAGCTACCGCAGAGTCTTCAGATCATGCTG 120

QY 1120 AGAGAGCTGGAGGCACCCATGCCATCTCAACCTCTTCCCGCCGCTTTACAAAGGGGA 1179

Db 121 AGAGAGCTGGAGGCACCCATGCCATCTCAACCTCTTCCCGCCGCTTTACAAAGGGGA 180

QY 1180 GCGTAAAGCCAGAGACACTTGTATCAAGGACACAGCAAGTCAAGGTTGGAGCAGTAG 1239

Db 181 GCGTAAAGCCAGAGACACTTGTATCAAGGACACAGCAAGTCAAGGTTGGAGCAGTAG 240

QY 1240 CTGGAGGACCTGTCTCCAGCTCAGGCTCTTCCCTCCACCACTTCAAGTCTTCTT 1299

Db 241 CTGGAGGACCTGTCTCCAGCTCAGGCTCTTCCCTCCACCACTTCAAGTCTTCTT 300

QY 1300 TCCGAGGCCCTGTCTCAGGTTGAGTGTCTGAGTCTCAACCGCAAGGGAACAAGTACT 1359

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RESULT 11

B1911195

LOCUS

DEFINITION

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mRNA sequence.

ACCESSION

B1911195

VERSION

B1911195.1 GI:16174808

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

1 (bases 1 to 796)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1532 row: d column: 06

High quality sequence start: 29

High quality sequence stop: 791.

Location/Qualifiers

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/note="Vector: pCMV-SF0RT6; Site 1: NotI; Site 2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

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this is a NIH_MGC Library."

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Matches 765; Conservative 0; Mismatches 7; Indels 5; Gaps 5;

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Qy 61 CCGCGCGCTCCCTCGCGCC -GAGCTTCGAGCCAGAGCGCTTCCTGGGGAGCGGCTC 119
Db 80 CCGCGCGCTCCCTCGCGCCCTGAGCTTCGAGCCAGAGCGCTTCCTGGGGAGCGGCTC 139

Qy 120 ATGGCTTTACAGTAGACCGCTTGCTCCTCGCGCTGGCTTGGCTCCACGCGCCGACGG 179
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CO646993
LOCUS
DEFINITION
ILLUMIGEN MCQ 39909 Katze MMPB2 Macaca mulatta cDNA clone
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CD8A (Hs.85258), mRNA sequence.
ACCESSION
CO646993.1 GI:50568487
VERSION
CO646993
KEYWORDS
Macaca mulatta (rhesus monkey)
SOURCE
Macaca mulatta
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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424 GTACTTCAGCCACTTCGTGCGGCTCTCTGCGAGGAGGCCACACGAGCGCCGCGCC 483
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727 CCTTTTACTGCAACCAACAGAAACGAGAGCTGTGTTGCAAA - TGTCCCGGCGCTGTGGTC 785
664 CCTTTTACTGCAACCAACAGAAACGAGAAACGTTTGCAAAATTGTCCAGGCGCTGTGGTC 723
785 AAATCGGGAGACAGCCCGAGCCTTCGCGGAGATAGTCTTAACCTGTGC - AACAGCCAC 844
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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library Homo sapiens cDNA clone TC11602 5' similar to Homo sapiens
CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 1,
mRNA sequence.
DN997301
DN997301.1 GI:66257128
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 704)
Birckett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.
High-throughput cloning of full-length human cDNAs directly from
cDNA libraries optimized for large and rare transcripts
Unpublished (2005)
Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.

6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 5prime forward vector primer, Origene
Technologies Inc.
Location/Qualifiers
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 3.3e-122;
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QY 117 GTCATGGCTTACAGTGACCGCTTGTCTCGCGCTGGCTTGTCTTCCACGCGCC 176
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QY 417 CTCACCTGAGGAGCTTCGCGCGAGAGAAAGAGGCTACTATTTCTGCTCGGCCCTGAGC 476
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QY 477 AACTCCATCATCTACTTCAGCCACTTCGTGCGCGCTTCTCTCCAGCAAGCCACCAAG 536
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QY 657 GCTCTGATATCTACTATCTGGGCGCCCTTGGCGCGGAGCTTGGGGCTCTTCTCCGTCA 716
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| QY | 50 | CCCCACCGGCTCCCGCGCCCTCCCTCGCGCCGAGCTTCGAGCCAAAGCAGCGTCTCGG | 109 | | |
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| DB | 607 | TCCCGGCGCTGTGGTCAATCGGGAGACAGCCAGCCTTTCGGGAGAGATAGCTCTAACC | 666 | | |
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| DB | 667 | CTGTGCAACAGCCACTACATTACTTCAAACTGAGATCCTTCTCTTTTGGAGGAGCAAGTC | 726 | | |
| QY | 889 | CTTCCTCTTTTCATTTTTTCCAGTCTTCCTCGCTGTGTAATTCATTCATCATGATTATTATTT | 948 | | |

| | | | |
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| Db | 727 | CTTCCTTTTCATTTTTTCCAGCTTCTCCTCGTGTATTCATTCATGATTATTATTTT | 786 |
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Search completed: May 30, 2006, 09:48:04
Job time : 9655 secs

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| 3 | 1006.5 | 96.5 | 708 | 2 | AX764523 | AX764523 Sequence |

Score: 1043.00

inter

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| Best Local Similarity: | 100.0% | Mismatches: | 0 |
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| Db | 120 | ATGGCCCTTACAGTGACCGCCTTGTCTCGCGCTGGCTTGTCTCCACGCGCCAGG | 179 |
| Qy | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
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| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 240 | CTGAAGTGCCAGGTGCTGTCTCCACCCGACGTGGGCTGCTGTGGCTCTTCCAGCGG | 299 |
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| Db | 300 | CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG | 359 |
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| Qy | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
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| Qy | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 |
| Db | 480 | TCCATCATGTACTTCAGCCACTTGTGCGGCTTCTCCGAGGAAAGCCACACGAGC | 539 |
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| Qy | 161 | ProGluAlaCysArgProAlaAlaGlyAlaGlyAsnArgArgValCysLysCys | 180 |
| Db | 600 | CCAGAGGGCTGCGCGCCAGCGCGGGGGGCGCAGGGAACCGAGACGTGTTGCAATGT | 659 |
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| SOURCE | Homo sapiens | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Qi,Y., Zhang,X. and Konigsberg,P.J. | | |
| AUTHORS | Gene therapy vectors having reduced immunogenicity | | |
| TITLE | Patent: WO 2004083404-A 28 30-SEP-2004; | | |
| JOURNAL | Isogenis, Inc. (US) | | |
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| Best Local Similarity: | 83.8% | Mismatches: | 1 |
| Query Match: | 96.5% | Indels: | 37 |
| DB: | 2 | Gaps: | 1 |
| US-10-804-763-3 (1-198) x CQ882036 (1-708) | | | |
| Qy | 1 | MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg | 20 |
| Db | 1 | ATGGCCCTTACAGTGACCGCCTTGTCTCGCGCTGGCTTGTCTCCACGCGCCAGG | 60 |
| Qy | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| Db | 61 | CCGAGCCAGTTCGGGTGTCCCGCTGGATCGGACCTGGAAACCTGGGGGACAGTGGAG | 120 |
| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 121 | CTGAAGTGCCAGGTGCTGTCTCCACCCGACGTGGGCTGCTGTGGCTCTTCCAGCGG | 180 |
| Qy | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
| Db | 181 | GGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG | 240 |
| Qy | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
| Db | 241 | GCCGAGGGGCTGGACACCCAGCGGTTCGCGGCAAGAGGTTGGGGGACACCTTCGTCTC | 300 |
| Qy | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn | 120 |
| Db | 301 | ACCTGACGACTTCCGCGGAGAGACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC | 360 |
| Qy | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 |
| Db | 361 | TCCATCATGTACTTCAGCCACTTGTGCGGCTTCTCCGAGGAAAGCCACACGAGC | 420 |
| Qy | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| Db | 421 | CCAGCGCGCGACCAACCAACCGCGCCACCAATCGCGCTCGCAGCCCTGTCCCTGCGC | 480 |
| Qy | 161 | ProGluAlaCysArgProAlaAlaGlyAlaGlyAsnArgArgValCysLysCys | 171 |
| Db | 481 | CCAGAGGGCTGCGCGCCAGCGCGGGGGGCGCAGGTCACACGAGGGGCTGAGACTTCGCC | 540 |
| Qy | 171 | ----- | ----- |
| Db | 541 | TGTGATATCTACATCTGGGCGCCCTTGTGCGGACTTGTGGGGTCTTCTCTCTGTCACTG | 600 |
| Qy | 172 | ----- | ----- |
| Db | 601 | GTTATCACCCCTTTACTGCAACCAACGAGGAAACCGAGACGTGTTGCAAAATGTCCTCCGCGCT | 660 |
| Qy | 184 | ValVallySerSerGlyAspLysProSerLeuSerAlaArgTyrVal | 198 |
| Db | 661 | GTGTCAAAATCGGAGACACAGCCAGCCCTTTCGGCGAGATACGTC | 705 |
| RESULT 3 | | | |
| Q882036 | 708 bp | DNA | linear |
| LOCUS | Sequence 40 from Patent WO02102852. | | PAT 25-JUN-2003 |
| DEFINITION | Q882036 | | |
| ACCESSION | Q882036.1 | GI:32258731 | |
| VERSION | Q882036.1 | GI:32258731 | |
| KEYWORDS | Homo sapiens (human) | | |
| SOURCE | Homo sapiens | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; | | |
| TITLE | Hominidae; Homo. | | |
| JOURNAL | Jakobsen,B.K. and Glick,M. | | |
| | Modified CD8 molecule, nucleic acid encoding said molecule, and | | |
| | their therapeutic use | | |
| | Patent: WO 02102852-A 40 27-DEC-2002; | | |

[illegible]

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Db      277  |CCCCAGGGGCTGGACACCCAGCGGTTCTCGGCGAAGAGTTGGGGGACACCTTCGTCTCTC 336
Qy      101  |ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      337  |ACCCCTGAGCACTCCGCGGAGAGAACAGAGGCTACTATTCTGCTCGGCCCTTGAGCAAC 396
Qy      121  |SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      397  |TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCTCTGCCAGGAGCCACACGACG 456
Qy      141  |ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      457  |CCAGCGCGCGACCAACACCGCGCCGCCACCATCGCGTCCGACGCCCTGTCCCTGGCG 516
Qy      161  |ProGluAlaCysArgProAlaAlaGlyAla----- 171
Db      517  |CCAGAGGCGTCCGCGGACAGCCAGCCCTTTTCGGCGGAGATACGTC 741
Db      697  |GTGGTCAATCGGAGACAGCCAGCCCTTTTCGGCGGAGATACGTC 741

RESULT 5
AX011079 LOCUS AX011079 773 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 16 from Patent WO9957266.
ACCESSION AX011079
VERSION AX011079.1 GI:9997709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Dörfling, A. and Lechler, I. R.
TITLE Immunosuppression by blocking t cell co-stimulation signal 2
(b7/cd28 interaction)
JOURNAL Patent: WO 9957266-A 16 11-NOV-1999;
IMP COLLEGE INNOVATIONS LTD (GB); DÖRLING ANTHONY (GB); LECHLER IAN
ROBERT (GB)
FEATURES
source Location/Qualifiers
1..773
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1..38e-65 Length: 773
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x AX011079 (1-773)

Qy      1  |MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      37  |ATGGCTTACAGTACCGGCTTGCTCTCGCGCTGGCGTCTGCTCCAGCCGCCAGG 96
Qy      21  |ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyLysThrValGlu 40
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Db      97  |CCGAGCCAGTTCGGGGTGTCCGCCCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 156
Qy      41  |LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      157  |CTGAAGTGCCAGGTGCTGCTGTCACACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 216
Qy      61  |ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      217  |CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCCAAAACAAGCCCAAGCG 276
Qy      81  |AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      277  |GCCAGGGGCTGGACACCCAGCGGTTTCGGGCGAAGAGTTGGGGGACACCTTCGTCTCTC 336
Qy      101  |ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      337  |ACCCCTGAGCACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 396
Qy      121  |SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db      397  |TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCTGCGGAGAACCCACACGACG 456
Qy      141  |ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      457  |CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTCCGACGCCCTGTCCCTGGCG 516
Qy      161  |ProGluAlaCysArgProAlaAlaGlyAla----- 171
Db      517  |CCAGAGGCGTCCGCGGACAGCCAGCCCTTTTCGGCGGAGATACGTC 741
Qy      171  |----- 171

Db      577  |TGTGATATCTACATCTGGGCGCCCTTGGCGGAGCTTGTGGGGTCTTCTCTGTCTACTG 636
Qy      172  |-----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db      637  |GTTATCACCTTTACTGCAACACAGGACCGAGACGTTTTCGCAATGTCTCCCGGCT 696
Qy      184  |ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      697  |GTGGTCAATCGGAGACAGCCAGCCCTTTTCGGCGGAGATACGTC 741

RESULT 6
CO725925 LOCUS CO725925 1059 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 11859 from Patent WO02068579.
ACCESSION CO725925
VERSION CO725925.1 GI:42287423
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Venter, C. J., Adams, M. C., Li, P. W. and Myers, E. W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
human exons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 11859 06-SEP-2002;
PE CORPORATION (NY) (US)
FEATURES
source Location/Qualifiers
1..1059
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 1.81e-65 Length: 1059
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
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Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x CQ725925 (1-1059)

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DB 65 ATGGCCCTTACAGTACCGCTTGTCTCCGCTGGCTTGTCTCCACGCCGCCAGG 124

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTriAsnLeuGlyGluThrValGlu 40
DB 125 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGACCTTGGAACTTGGCGGAGACAGTGGAG 184

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 185 CTGAAGTGCAGGTGCTGCTCCAAACCCGACGCTGGGCTGTCTGGCTTCTCCAGCCG 244

QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
DB 245 CGCGGGCGCGCCAGTCCACCTTCTCTATAGCTCTCCCAAAACAAGCCCAAGGCG 304

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 305 GCGAGGGGCTGGACACCGCGGTCTCGGCAAGAGGTGGGGGACACCTTCGTCTC 364

QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrPheCysSerAlaLeuSerAsn 120
DB 365 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGACCAAC 424

QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 425 TCCATCATGTACTTACGACCTTCGTGCGGCTTCTGCGCAGGAGGCTGTCTCCCTGCGC 484

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 485 CAGCGCCGCGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCCCTGCGC 544

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 545 CCAGAGCGGTGCGCGCGAGCGGGGCGGCGAGTGCACAGAGGGGCTGGACTTCGCC 604

QY 171 ----- 171

DB 605 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTCTGTCTC 664

QY 172 ----- 171

DB 665 GTTATCACCTTTACTGCAACCCACAGAACCCGAGACGTGTTTGCATAATGTCCCCGCGCT 724

QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyTrVal 198
DB 725 GTGGTCAATTCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 769

RESULT 7
LOCUS 123895
DEFINITION Sequence 11 from patent US 5540926.
ACCESSION 123895
VERSION 123895.1 GI:1603765
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Aruffo,A., Hollenbaugh,D. and Ledbetter,J.A.
TITLE Soluble and its use in B cell stimulation
JOURNAL Patent: US 5540926-A 11 30-JUL-1996;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN

Alignment Scores: 1.81e-65 Length: 1060
Pred. No.: 1006.50 Matches: 197
Score: 83.8% Conservatives: 0
Percent Similarity: 83.8% Mismatches: 1
Best Local Similarity: 96.5% Indels: 37
Query Match: 96.5% Gaps: 1
DB: 2

US-10-804-763-3 (1-198) x 123895 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 66 ATGGCCCTTACAGTACCGCTTGTCTCCGCTGGCTTGTCTCCACGCCGCCAGG 125

QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTriAsnLeuGlyGluThrValGlu 40
DB 126 CCGAGCCAGTTCGGGTGTCCCGCTGGATCGACCTTGGAACTTGGCGGAGACAGTGGAG 185

QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 186 CTGAAGTGCAGGTGCTGCTCCAAACCCGACGCTGGGCTGTCTGGGTCTTCTCCAGCCG 245

QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
DB 246 CGCGGGCGCGCCAGTCCACCTTCTCTATAGCTCTCCCAAAACAAGCCCAAGGCG 305

QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 306 GCGAGGGGCTGGACACCGCGGTCTCGGCAAGAGGTGGGGGACACCTTCGTCTC 365

QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrPheCysSerAlaLeuSerAsn 120
DB 366 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGACCAAC 425

QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 426 TCCATCATGTACTTACGACCTTCGTGCGGCTTCTGCGCAGGAGGCTGTCTCCCTGCGC 485

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CAGCGCCGCGACCAACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCCCTGCGC 545

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 546 CCAGAGCGGTGCGCGCGAGCGGGGCGGCGAGTGCACAGAGGGGCTGGACTTCGCC 605

QY 171 ----- 171

DB 605 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTCTGTCTC 665

QY 172 ----- 171

DB 666 GTTATCACCTTTACTGCAACCCACAGAACCCGAGACGTGTTTGCATAATGTCCCCGCGCT 725

QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyTrVal 198
DB 726 GTGGTCAATTCGGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 8
LOCUS AR380469
DEFINITION Sequence 1014 from patent US 6607879.
ACCESSION AR380469
VERSION AR380469.1 GI:40088103
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1060)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 1014 19-AUG-2003;

| | | |
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| ORGANISM | Homo sapiens | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | |
| AUTHORS | 1 (bases 1 to 1060) | |
| TITLE | Littman,D.R., Thomas,Y., Maddon,P.J., Chess,L. and Axel,R. | |
| JOURNAL | The isolation and sequence of the gene encoding T8: a molecule defining functional classes of T lymphocytes | |
| PUBMED | Cell 40 (2), 237-246 (1985) | |
| COMMENT | 3871356 | |
| FEATURES | Original source text: Human peripheral T cell, cDNA to mRNA, clones pT8.B and pT8.F1. | |
| source | Location/Qualifiers | |
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| CDS | 1..65 | |
| | 66..773 | |
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| | /db_xref="GI:179146" | |
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| mat_peptide | 126..770 | |
| | /product="cell surface glycoprotein T8" | |
| 3'UTR | 774..1060 | |
| ORIGIN | | |
| Alignment Scores: | | |
| Pred. No.: | 1.81e-65 | |
| Score: | 1006.50 | |
| Percent Similarity: | 83.8% | |
| Best Local Similarity: | 83.8% | |
| Query Match: | 96.5% | |
| DB: | 5 | |
| | Gaps: 1 | |
| | US-10-804-763-3 (1-198) x HUMATCT8A (1-1060) | |
| QY | 1 | MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiaAlaAarg 20 |
| Db | 66 | ATGGCCTTACCAAGTACCGCCTTGCTCTCGCGCTGGCCTTGCTCTCCAGCGCCGACG 125 |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40 |
| Db | 126 | CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGACCTGGAACCTGGCGGAGACAGTGGAG 185 |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60 |
| Db | 186 | CTGAAGTCCAGGTCTGCTGTCCAAACCGACGCTGGGCTGCTCGTGGCTCTTCCAGCGC 245 |
| QY | 61 | ArgGlyAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80 |
| Db | 246 | CGCGGCGCGCGCGAGTCCACCTTCCTCTATACCTCTCCAAAACAAGCCCAAGGCG 305 |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100 |
| Db | 306 | GCCGAGGGGCTGGACACCCAGCGGTTCGGCGCAAGAGGTTGGGGGACACCTTCGCTC 365 |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120 |
| Db | 366 | ACCTTGACGACTTCGCGGAGAGACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 425 |
| QY | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140 |
| Db | 426 | TCCATCATGTACTTCAGCCACTTCGTGCGGGTCTTCTCTGCCAGGAGCCACCGACG 485 |
| QY | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160 |
| Db | 486 | CCAGGCGCGGACCAACCAACCGCGCGCCACCATCGGCTGCGAGCCCTGTCTCTCGGC 545 |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171 |
| Db | 546 | CCAGAGGCGTGCAGCGCGCGCGCGCGCAGTGCACACAGGGGCGTGGACTTCGCC 605 |
| QY | 171 | ----- 171 |
| Db | 606 | TGTGATATCTACATCTGGGCGCCCTTGGCGGGAGCTTGTGGGGTCCCTTCTCTGTCACTG 665 |
| QY | 172 | -----GlyAsnArgArgArgValCysLysCysProArgPro 183 |
| Db | 666 | GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGCTGTTTGCAAATGTCCCCGSCCT 725 |
| QY | 184 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198 |
| Db | 726 | GTGGTCAATCGGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 770 |
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| HUMATCT8A | | |
| LOCUS | 1060 bp | mRNA |
| DEFINITION | Homo sapiens T-cell surface protein T8 mRNA. | PRI 22-JUL-1996 |
| ACCESSION | M12828 | |
| VERSION | M12828.1 | GI:179145 |
| KEYWORDS | cell surface glycoprotein. | |
| SOURCE | Homo sapiens (human) | |

JOURNAL Patent: WO 2004083404-A 2 30-SEP-2004;

Isogenis, Inc. (US)

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.: 3,49e-65 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x CQ882010 (1-2261)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 120 ATGGCTTACCAGTACCGGCTTCTCTCGCGCTGGCTTGTCTCCAGCGGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyValGlu 40
Db 180 CCGAGCCAGTTCGCGGCTGGATCGGACCTGGAACCTGGGCGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGCTCCAAACCGAGCTCGGGCTGCTGTGCTCTCCAGCG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCCCAAAACCAAGCCCAAGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGGACACCTTCTGCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGGCACCTTCGTGCGGCTTCTCTGCCAGCAAGCCACCAAGCG 539
Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCAACACCGCGGCCACCATCGCGTTCGCGGCAAGCCCTGTCCCTGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 600 CCAGAGGCGTGGCGGCGCGCGCGGGCGGAGTGCACACGAGGGGGTGGACTTCGCG 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGCTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATACCTTTTACTGCAACACAGGAAACCAAGACGTTTGCAAAATGTCCTCCCGGCT 779
Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAATCGGAGACAAAGCCAGCCTTTTCGGCGAGATACGTC 824

RESULT 12

AX764527

LOCUS

Sequence 44 from Patent WO201202852.

DEFINITION

AX764527

ACCESSION

AX764527.1 GI:32258735

linear

PAT 25-JUN-2003

KEYWORDS

synthetic construct
synthetic construct
other sequences; artificial sequences.

REFERENCE

1

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

Location/Qualifiers

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1..708

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RPVVKSGDKFSLSARYV"

ORIGIN

Alignment Scores:

Pred. No.: 2,13e-65 Length: 708

Score: 1003.50 Matches: 196

Percent Similarity: 83.8% Conservatives: 1

Best Local Similarity: 83.4% Mismatches: 1

Query Match: 96.2% Indels: 37

DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x AX764527 (1-708)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyValGlu 40

Db 61 CCGAGCCAGTTCGCGGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 120

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60

Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCGAGCTCGGGCTGCTGTGCTCTTCCAGCG 180

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80

Db 181 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCAACCAAAACCAAGCCCAAGCG 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100

Db 241 GCCGAGGGGCTGGACACCGCGGTTCTCGGCAAGAGTTGGGGGACACCTTCTGCTC 300

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120

Db 301 ACCCTGAGGACTTCCCGCGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 360

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140

Db 361 TCCATCATGTACTTCAGGCACCTTCGTGCGGCTTCTCTGCCAGCAAGCCACCAAGCG 420

Qy 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 421 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTCGCGACGCCCTGTCCCTGCGC 480

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171

Db 481 CCAGAGGCGTGGCGGCGCGCGGGGCGCAGTGCACACGAGGGGGCTGGACTTCGCG 540

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QY      171 ----- 171
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QY      172 -----GlyAsnArgArgValCysLysCysProArgPro 183
Db      601 GTTATCACCTTTACTGCAACACACAGAACCGAAGACGTGTTTGCAAAATGTCCTCCGGCCT 660
QY      184 ValVallySerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      661 GTGTCAAATCGGAGACAGCCAGCCCTTTCGGCGAGATACGTC 705

RESULT 13
AY039664
LOCUS      1018 bp mRNA linear PRI 17-JUL-2001
DEFINITION Homo sapiens mutant CD8 alpha antigen (CD8A) mRNA, complete cds.
ACCESSION AY039664
VERSION    AY039664.1 GI:14861039
KEYWORDS
SOURCE
ORGANISM   Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS   de la Calle-Martin,O., Hernandez,M., Ordi,J., Casamitjana,N.,
Rodriguez-Sanchez,J.L. and Espanol,T.
Famillial CD8 deficiency due to a mutation in the CD8 alpha gene
J. Clin. Invest. 108 (1), 117-123 (2001)
11435463
TITLE     2 (bases 1 to 1018)
JOURNAL   Casamitjana,N., Arostegui,J.I. and de la Calle,O.
PUBMED   Direct Submission
REFERENCE Submitted (12-JUN-2001) Immunohematology, Centre de Transfusio i
AUTHORS   Banc de Teixits, Pg. de la Vall d'Hebron 119-129, Barcelona 08035,
JOURNAL   Spain
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Alignment Scores:
Pred. No.:      4,87e-65      Length:      1018
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Percent Similarity: 83.4%      Conservative: 0
Best Local Similarity: 83.4%      Mismatches: 37
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US-10-804-763-3 (1-198) x AY039664 (1-1018)

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    |||||
240 CCGAGCCAGTTTCGGGTGTTCGGCTGGATCGGACCTGGAAACCTGGCGCGAGACAGTGGAG 299
QY      41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrPheGlnPro 60
    |||||
300 CTGAAGTGCAGGTGCTGCTGTCCAAACCCAGAGTCGGGCTGCTGTGGTCTCTTCCAGCCG 359
QY      61 ArgGlyAlaAlaAserProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
    |||||
360 CGCGGCGCGCGCGCAGTCCCACCTTCTCTCTATACCTCTCCCAAAACAAGCCCAAGCGG 419
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420 GCCGAGGGGCTGGACACCCAGCGGTTCGGGCAAGAGGTTGGGGACACCTTCTGTCCTC 479
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480 ACCCTGAGGAGACTTCGCGCGAGAGAACGAGAGCTACTATTTCTGCTCGGCCCTTGACCAAC 539
QY      121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
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540 TCCATCATGTACTTTCAGGCACCTTCGTGCGCGTCTTCTCCAGCAGGAAGCCACCCAGCAG 599
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RESULT 14
BC025715
LOCUS      2150 bp mRNA linear PRI 29-JUN-2004
DEFINITION Homo sapiens CD8 antigen, alpha polypeptide (p32), transcript
variant 1, mRNA (cDNA clone MGC:34614 IMAGE:5227906), complete cds.
ACCESSION BC025715
VERSION    BC025715.1 GI:193444021
KEYWORDS   MGC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2150)
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

```

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

12477932

JOURNAL

2 (bases 1 to 2150)

PUBMED

Strausberg,R.

REFERENCE

Direct Submission

AUTHORS

Submitted (06-MAR-2002) National Institutes of Health, Mammalian

TITLE

Gene Collection (MGC), Cancer Genomics Office, National Cancer

JOURNAL

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT

Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov
 Akter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
 Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
 Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
 Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laxic,P., Legaspi,R.,
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 Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,B.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAP Plate: 49 Row: 0 Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 27886641.

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ORIGIN

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

Alignment Scores:

Pred. No.: 1.55e-64 Length: 2150
 Score: 997.50 Matches: 196
 Percent Similarity: 83.4% Conservative: 0
 Best Local Similarity: 83.4% Mismatches: 2
 Query Match: 95.6% Indels: 37
 DB: 5 Gaps: 1

US-10-804-763-3 (1-198) x BC025715 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
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 Db |||||
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CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

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AUTHORS

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LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

CQ843147

LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

CQ843147

ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

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LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

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VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

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LOCUS

Sequence 1794 from Patent EP1440981.

DEFINITION

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ACCESSION

VERSION

CQ843147.1 GI:50894934

KEYWORDS

Homo sapiens (human)

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

1 Isogai,T., Sugiyama,T., Otauki,T., Wakamatsu,A., Sato,H., Ishii,S.,

AUTHORS

Yamamoto, J., Isono, Y., Nagai, K. and Irie, R.

Full-length human cDNA

Patent: EP 1440981-A 1794 28-JUL-2004;

Research Association for Biotechnology (JP)

FEATURES

Location/Qualifiers

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| Query Match: | 95.4% | Indels: | 37 |
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US-10-804-763-3 (1-198) x CQ843147 (1-3048)

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Db      1092 CCGAGCCAGTTCGGCGGTGCGCGCTGGATCGGACCTGGGCGAGACAGTGGAG 1151
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Db      1512 CCAGAGGGGTGCGCGCCAGCGCGGGCGCGAGTGCAACGAGGGGGTGGACTTCGCC 1571
QY      171 ----- 171
Db      1572 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTGTCACTG 1631
QY      172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db      1632 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGAGGTGTTTGCAATGTCCCCGGCCT 1691
QY      184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      1692 GTGGTCAATCGGAGACAAGGCCAGCCCTTTCGGCGAGATAGTC 1736

```

Search completed: May 30, 2006, 07:16:35

Job time : 5111.02 secs

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 29, 2006, 22:39:21 ; Search time 762.277 Seconds
(without alignments)
2716.542 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSRVV 198

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THRM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02p
-USER=US10804763 @CGN 1 1 2295 @runat_26052006.165049.14393 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1043 | 100.0 | 2150 | 13 | Ad92793 CDNA of a |
| 2 | 1043 | 100.0 | 2150 | 13 | Ad92793 Human sec |
| 3 | 1043 | 100.0 | 2150 | 14 | Ad226403 Human CD8 |

| | | | | | | |
|----|--------|-------|------|----|----------|--------------------|
| 4 | 1043 | 100.0 | 3518 | 14 | AED96282 | Aed96282 Human C-r |
| 5 | 1006.5 | 96.5 | 708 | 2 | AAx80967 | Aax80967 Human CD8 |
| 6 | 1006.5 | 96.5 | 708 | 8 | ABz69260 | Abz69260 Human CD8 |
| 7 | 1006.5 | 96.5 | 708 | 13 | ADS92817 | Ad92817 Nucleotid |
| 8 | 1006.5 | 96.5 | 708 | 13 | ADS19462 | Ad92817 Nucleotid |
| 9 | 1006.5 | 96.5 | 708 | 14 | ADW42461 | Adw42461 Coding se |
| 10 | 1006.5 | 96.5 | 708 | 15 | ASF68357 | Ase68357 Human psy |
| 11 | 1006.5 | 96.5 | 1060 | 2 | AAQ57986 | Aaq57986 Genomic s |
| 12 | 1006.5 | 96.5 | 1060 | 10 | ADD25612 | Add25612 Binding d |
| 13 | 1006.5 | 96.5 | 1060 | 11 | ADI31688 | Adi31688 Human CDN |
| 14 | 1006.5 | 96.5 | 1060 | 13 | ADS83755 | Ad83755 Human lym |
| 15 | 1006.5 | 96.5 | 2123 | 10 | ADP90782 | Adp90782 Human hep |
| 16 | 1006.5 | 96.5 | 2261 | 12 | ADP10406 | Adp10406 Reference |
| 17 | 1006.5 | 96.5 | 2261 | 13 | ADS92791 | Ad92791 Nucleotid |
| 18 | 1006.5 | 96.5 | 2261 | 13 | ADS19437 | Ad92791 Nucleotid |
| 19 | 1006.5 | 96.5 | 2261 | 14 | ADW86779 | Adw86779 DNA of th |
| 20 | 1006.5 | 96.5 | 2261 | 14 | ADZ26401 | Adz26401 Human CD8 |
| 21 | 1003.5 | 96.2 | 708 | 8 | ABz69262 | Abz69262 Human CD8 |
| 22 | 995.5 | 95.4 | 3048 | 12 | ADQ64633 | Adq64633 Novel hum |
| 23 | 987.5 | 94.7 | 773 | 3 | AAZ29002 | Aaz29002 Human CD8 |
| 24 | 909 | 87.2 | 2134 | 12 | ADQ22926 | Adq22926 Human sof |
| 25 | 899 | 86.2 | 662 | 12 | ADN11772 | Adn11772 Human CD8 |
| 26 | 899 | 86.2 | 1131 | 3 | AAZ46253 | Aaz46253 cDNA enco |
| 27 | 899 | 86.2 | 1837 | 12 | ADN11778 | Adn11778 CD8-SA/B- |
| 28 | 899 | 86.2 | 2909 | 12 | ADN11779 | Adn11779 CD8-NS2/3 |
| 29 | 899 | 86.2 | 4392 | 14 | AED96283 | Aed96283 Human C-r |
| 30 | 869.5 | 83.4 | 708 | 13 | ADS92815 | Ad92815 Nucleotid |
| 31 | 869.5 | 83.4 | 708 | 13 | ADS19461 | Ad92815 Nucleotid |
| 32 | 816.5 | 78.3 | 3407 | 14 | AED96285 | Ad92815 DNA of th |
| 33 | 816.5 | 78.3 | 3743 | 14 | AED96281 | Aed96285 Human C-r |
| 34 | 804 | 77.1 | 597 | 13 | ADS92795 | Aed96281 Human C-r |
| 35 | 804 | 77.1 | 597 | 13 | ADS19441 | Ad92795 Nucleotid |
| 36 | 782 | 75.0 | 3476 | 14 | AED96284 | Ad92795 Nucleotid |
| 37 | 637 | 61.1 | 366 | 2 | AAx80968 | Aed96284 Human C-r |
| 38 | 634 | 60.8 | 363 | 8 | ABz69261 | Aax80968 Expressed |
| 39 | 620.5 | 59.5 | 785 | 13 | ADS92811 | Abz69261 Human CD8 |
| 40 | 620.5 | 59.5 | 785 | 13 | ADS19457 | Ad92811 Nucleotid |
| 41 | 532 | 51.0 | 2001 | 13 | ADS92807 | Ad92811 DNA of th |
| 42 | 532 | 51.0 | 2001 | 13 | ADS19453 | Ad92807 Nucleotid |
| 43 | 510.5 | 48.9 | 1330 | 13 | ADS92805 | Ad92807 DNA of th |
| 44 | 510.5 | 48.9 | 1330 | 13 | ADS19451 | Ad92805 Nucleotid |
| 45 | 471.5 | 45.2 | 922 | 6 | ABU34273 | Ad92805 Nucleotid |
| C | | | | | | Ad92805 DNA of th |
| | | | | | | AB134273 Human imm |

ALIGNMENTS

RESULT 1
ADS92793
ID ADS92793 standard; cDNA; 2150 BP.

XX ADS92793;

XX AC ADS92793;

XX DT 16-DEC-2004 (first entry)

XX DE cDNA of a secreted CD8 alpha-chain protein alternative transcript.

XX KW immune response; cell-specific antigen; alloantigen; CD8;

XX KW CD8 alpha-chain; cellular immune response; humoral immune response;

XX KW transplant allograft; graft-versus-host disease; transplant; gene; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 120..716

XX FT /*tag= a

XX FT /product= "CD8 alpha-chain"

XX PN WO2004083244-A2.

XX PD 30-SEP-2004.

XX XX 19-MAR-2004; 2004WO-US008574.

XX PF

using related

```
PR 19-MAR-2003; 2003US-0456378P.
XX (ISOG-) ISOGENIS INC.
XX Qi Y, Zhang X, Konigsberg PJ;
XX WPI; 2004-691022/67.
XX P-PSDB; ADS92792.
XX Specifically inhibiting host immune responses to alloantigens, useful for
PT e.g. treating graft-versus-host disease, comprises contacting a target
PT cell expressing the antigen with an expression vector encoding a CD8
PT polypeptide.
XX
XX Disclosure; Fig 1; 98pp; English.
XX The specification describes a method for specifically inhibiting a host
CC immune response to target cell-specific antigens (e.g. alloantigens). The
CC method comprises contacting a target cell expressing the antigen with an
CC expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
CC chain, where the CD8 polypeptide is expressed by the target cell and
CC where the host immune response against the target cell is specifically
CC inhibited. The method of the invention is useful for specifically
CC inhibiting both cellular and humoral immune responses to alloantigens.
CC thus finding use in extending the survival of transplant allografts and
CC in treating graft-versus-host disease in transplant recipients. The
CC present sequence encodes an alternative transcript of a secreted alpha-
CC chain of a CD8 protein. This CD8 alpha-chain may be used in the method of
CC the invention.
XX
XX SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.82e-67 Length: 2150
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-3 (1-198) x ADS92793 (1-2150)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCTTACAGTACCGCTTGTCTCGCGCTGGCTTGTCTCTCCAGCCGCCAGG 179
QY 21 ProSerGlnPheAtqValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTGTGCGCGTGGATCGGACCTGGACCTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTCTGTCTCCAAACCGACGCTGGGCTGTCTGTGGCTCTTCCAGCG 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 300 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCGAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCTCTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGCGCCCTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 480 TCCATCATGTACTTCCAGCCACTTCTGTCGGGTCTTCTGCGGAGGAGGCCACCCACGAG 539
QY 141 ProAlaProAtqProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCCACCAACACCGCGGCCACCATCGCGTGGCGCCCTGTCTCTGCGC 599
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QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgArgValCysLysCys 180
Db 600 CCAGAGCGGTGCCCGCCAGCGCGGGGGCCGAGGAAACCGAAGACGTGTTTGCATAATGT 659
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 660 CCCCGGCTGTGTCAATCGGGAGACNAGCCAGCCCTTTCGGCGAGATACGTC 713
```

```
RESULT 2
ADSI9439
ID ADSI9439 standard; DNA; 2150 BP.
AC ADSI9439;
XX 16-DEC-2004 (first entry)
XX Human secreted protein related to CD8 alpha chain DNA.
XX human; gene; ds; gene therapy; CD8 alpha chain; cellular immune response;
KW humoral immune response; immunosuppressive.
XX Homo sapiens.
XX Key Location/Qualifiers
FT CDS 120..716
FT /*tag= a
FT /product= "CD8 alpha chain related protein"
XX WO2004083404-A2.
XX 30-SEP-2004.
XX 19-MAR-2004; 2004WO-US008567.
XX 19-MAR-2003; 2003US-0456378P.
XX (ISOG-) ISOGENIS INC.
XX Qi Y, Zhang X, Konigsberg PJ;
XX WPI; 2004-691049/67.
XX P-PSDB; ADS19438.
XX New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
operably linked to a nucleic acid encoding a transmembrane polypeptide,
PT useful for inhibiting cellular and humoral components of the host immune
PT responses.
XX Disclosure; Fig 1; 94pp; English.
```

This invention relates to novel gene therapy vectors with reduced immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8 alpha chain operably linked to nucleic acid encoding a transmembrane polypeptide and a second nucleic acid representing the therapeutic gene of interest (for example ornithine carbamoyl transferase or beta glucosidase), whereby transcriptional and translational control elements direct expression thereof. The present invention describes a method to reduce an immune response against antigens derived from a gene therapy delivery system i.e. improving the expression of a therapeutic transgene in a host and improving viral expression vectors with reduced immunogenicity. Accordingly, these compositions are useful for inhibiting both the cellular and humoral components of the host immune responses against expression vectors and target cells transfected with the vectors. As such, they exhibit immunosuppressive activity. This polynucleotide is the DNA sequence of a human secreted protein (derived from an alternate transcript) related to the CD8 alpha chain of the invention.

SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.82e-67 Length: 2150
Score: 1043.00 Matches: 198

numbers / date

Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-804-763-3 (1-198) x ADS19439 (1-2150)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 120 ATGGCCTTACCACTGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCAGCCAGTTCGGGTGCGCGCTGGATCGGACTTGGAACTTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTCTCAACCCGACGCTGGGTGCTGTGGTCTTCCAGCGG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAla 80
DB 300 CGCGCGCGCGCGCCAGTCCACCTTCTCTATATCTCTCCCAAAACAAGCCCAAGCGG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCAGGGGCTGACACCCAGCGGTTCGCGGCAAGAGGTGGGGGACACCTTGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCCCGAGAGACGAGGGCTACTATTCTGTCTCGGCTTGACCA 479
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCCAGCAAGCCACCAAGCG 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGCGCCACCAACCGCGCGCCACCATCGCGTCCGAGCGCCCTGTCCCTG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
DB 600 CCAGAGGCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 659
QY 181 ProArgProValLysSerGlyAspLysProSerLeuSerAlaArgTyTrVal 198
DB 660 CCCCCTGTGTGTCAAATCGGAGACAAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 3

ADZ26403
ID ADZ26403 standard; cDNA; 2150 BP.

XX AC ADZ26403;

XX DT 16-JUN-2005 (first entry)

XX DE Human CD8 cDNA.

XX KW cell culture; stem cell; CD8; ss; gene.

XX OS Homo sapiens.

XX PN WO2005030999-A1.

XX PD 07-APR-2005.

XX PF 24-SEP-2004; 2004WO-US031524.

XX PR 25-SEP-2003; 2003US-0506221P.

XX PR 08-OCT-2003; 2003US-0509594P.

XX PA (DAND) DANA FARBER CANCER INST INC.

XX PI Ritz J, Wu CJ;

XX WPI; 2005-273394/28.
DR P-PSDB; ADZ26404.

XX Detecting lineage-specific cells in a biological sample, useful for
PT determining the clinical outcome of a progenitor cell transfer in a
PT subject, comprises identifying lineage-specific mRNA in the sample.

XX Disclosure; SEQ ID NO 29; 393pp; English.

XX The invention relates to a method of detecting lineage-specific cells in
CC a biological sample which comprises identifying lineage-specific mRNA in
CC the sample. The methods are useful for determining the clinical outcome
CC of a progenitor cell transfer in a subject, and for identifying or
CC quantifying lineage-specific cells. The present sequence represents a
CC human cDNA that encodes a protein used to identify lineage-specific
CC cells.

SQ Sequence 2150 BP; 609 A; 565 C; 501 G; 475 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1-82e-67 Length: 2150
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0


US-10-804-763-3 (1-198) x ADZ26403 (1-2150)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 120 ATGGCCTTACCACTGACCGCTTGTCTCGCGCTGGCTTGTCTCCACGCGCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCAGCCAGTTCGGGTGTCGCCGCTGGATCGGACTTGGAACTTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTGCTGTCTCCAAACCCGACGCTGGGTGCTGTGGTCTTCCAGCGG 299
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAla 80
DB 300 CGCGCGCGCGCGCCAGTCCACCTTCTCTATATCTCTCCCAAAACAAGCCCAAGCGG 359
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCCAGGGGCTGACACCCAGCGGTTCGCGGCAAGAGGTGGGGGACACCTTGTCTC 419
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
DB 420 ACCCTGAGCGACTTCGCCCGAGAGACGAGGGCTACTATTCTGTCTCGGCTTGACCA 479
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 480 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCAAGCCACCAAGCG 539
QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCGCGCGCCACCAACCGCGCGCCACCATCGCGTCCGAGCGCCCTGTCCCTG 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys 180
DB 600 CCAGAGGCGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 659
QY 181 ProArgProValLysSerGlyAspLysProSerLeuSerAlaArgTyTrVal 198
DB 660 CCCCCTGTGTGTCAAATCGGAGACAAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 4

AED96282
ID AED96282 standard; DNA; 3518 BP.

XX AC AED96282;
XX DT 26-JAN-2006 (first entry)
XX DE Human C-reactive protein (CRP) associated marker DNA SEQ ID NO 439.
XX KW Cardiant; Cerebroprotective; Vasotropic; Dermatological; Antiarthritic;
XX KW Antirheumatic; Antiinflammatory; Anticoagulant; Antimicrobial;
XX KW Immunosuppressant; cardiovascular-gen.; myocardial infarction;
XX KW Cardiovascular disease; coronary artery disease;
XX KW cerebrovascular ischemia; peripheral vascular disease;
XX KW congestive heart failure; sudden cardiac death;
XX KW C-reactive protein pentraxin-related; CRP; genetic marker; ds.
XX OS Homo sapiens.
XX PN WO2005107364-A2.
XX PD 17-NOV-2005.
XX PF 27-JAN-2005; 2005WO-IB002407.
XX PR 27-JAN-2004; 2004US-0539128P.
XX PR 27-JAN-2004; 2004US-0539129P.
XX PR 22-OCT-2004; 2004US-0620874P.
XX PR 22-OCT-2004; 2004US-0621004P.
XX PR 25-OCT-2004; 2004US-0621053P.
XX PR 25-OCT-2004; 2004US-0621072P.
XX PR 26-OCT-2004; 2004US-0621663P.
XX PR 27-OCT-2004; 2004US-0622016P.
XX PR 27-OCT-2004; 2004US-0622017P.
XX PR 17-NOV-2004; 2004US-0622320P.
XX PR 17-NOV-2004; 2004US-0628101P.
XX PR 17-NOV-2004; 2004US-0628112P.
XX PR 17-NOV-2004; 2004US-0628133P.
XX PR 17-NOV-2004; 2004US-0628134P.
XX PR 17-NOV-2004; 2004US-0628144P.
XX PR 17-NOV-2004; 2004US-0628145P.
XX PR 17-NOV-2004; 2004US-0628156P.
XX PR 17-NOV-2004; 2004US-0628165P.
XX PR 17-NOV-2004; 2004US-0628179P.
XX PR 17-NOV-2004; 2004US-0628190P.
XX PR 17-NOV-2004; 2004US-0628231P.
XX PR 17-NOV-2004; 2004US-0628251P.
XX PR 26-NOV-2004; 2004US-0630559P.
XX PR 08-DEC-2004; 2004US-0634075P.
XX PR 27-JAN-2005; 2005US-00043806.
XX PA (COMP-) COMPUEN LTD.
XX PA (COHE/) COHEN Y.
XX PI Toporik A, Pollock S, Levine Z, Avalon-Soffer M, Cojocaru GS;
XX PI Diber A, Novik A, Dahary D, Akiva P, Sorek R, Shemesh R;
XX DR WPI; 2005-810779/82.
XX PT New polynucleotide, useful for diagnosing a CRP variant-detectable
XX PT disease or for selecting therapy for a CRP variant-detectable disease,
XX PT e.g., myocardial infarction, coronary artery disease.
XX PS Disclosure; SEQ ID NO 439; 1670pp; English.
XX CC The invention relates to a new isolated polynucleotide. The
XX CC polynucleotide is useful for diagnosing a CRP variant-detectable disease,
XX CC for monitoring disease progression or treatment efficacy or relapse of a
XX CC CRP variant-detectable disease or for selecting therapy for a CRP variant
XX CC -detectable disease, e.g., myocardial infarction, coronary artery
XX CC disease, non-fatal or fatal stroke, peripheral vascular disease,
XX CC congestive heart failure or sudden cardiac death. The present sequence
XX CC represents a human C-reactive protein, pentraxin-related (CRP) associated
XX CC marker DNA.

SQ Sequence 3518 BP; 766 A; 1056 C; 907 G; 789 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 3.18e-67 Length: 3518
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 14 Gaps: 0
US-10-804-763-3 (1-198) x AED96282 (1-3518)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaArg 20
Db 1608 ATGCCCTTACCAGTGACCGCCTTCTCTCGCGTGGCTTGGCTCTCCAGCCCGAGG 1667
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAenLeuGlyGluThrValGlu 40
Db 1668 CCGAGCCAGTTCGGGTGTGCGCGCTGGATCGGACCTGGGACGACAGTGGAG 1727
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 1728 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTGCTGCTCTCCAGCCG 1787
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrlfueSerGlnAsnLysProLysAla 80
Db 1788 CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAAACAAAGCCCAAGCGG 1847
Qy 81 AlaGlyGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 1848 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCCTCTC 1907
Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrlfuePheCysSerAlaLeuSerAsn 120
Db 1908 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 1967
Qy 121 SerileMetTyrlfueSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 1968 TCCATCATGTACTTCCAGCCACTTCTGTCGGTTCCTCGCCAGCAAGCCACACGAGC 2027
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 2028 CCAGCGCGCGACCAACACCGCGGCCACCATCGGTGCGACGCCCTGTCTCCCTGCGC 2087
Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaGlyAlaGlyAsnArgArgValCysLysCys 180
Db 2088 CCAGAGCGTCCGCGCCAGCGCGCGGGGGCGCAGGAAACCGAAGACGTGTTTGCAATGT 2147
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrlVal 198
Db 2148 CCCCAGCGCTGTGTCAATCGGAGACAAAGCCAGCCCTTTCGGCGAGATACGTC 2201
RESULT 5
AXX80967
ID AXX80967 standard; cDNA; 708 BP.
XX AC AXX80967;
XX DT 18-AUG-1999 (first entry)
XX DE Human CD8 alpha protein encoding cDNA.
XX KW T lymphocyte inhibition; CD8; immunosuppressive therapy; transplantation;
XX KW autoimmune disease; allergy; asthma; viral infection; cytotoxic;
XX KW corticosteroid; human; CD8 alpha protein; ss.
XX OS Homo sapiens.
XX PN WO9921576-A1.
XX PD 06-MAY-1999.
XX PR 28-OCT-1998; 98WO-GB003235.


XX 28-OCT-1997; 97GB-00022779.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Jakobsen BK, Gao GF, Gerth UC, Sewell AK;
 XX WPI; 1999-385058/32.
 XX P-PSDB; AAV21688.
 XX Inhibiting activity of T cells against target cells useful for treating
 PT autoimmune diseases and allergy.
 XX Disclosure; Fig 1A; 79pp; English.
 XX The invention describes a method for inhibiting activity of T lymphocytes
 CC against a target cell by treating the cell with a soluble form of a CD8
 CC molecule. The method is used as immunosuppressive therapy, e.g. in
 CC patients undergoing transplantation, but also for treating autoimmune
 CC diseases and allergy, e.g. exacerbation of asthma caused by viral
 CC infection. The CD8 protein inhibits cytotoxic T cells in vitro or in
 CC vivo, amnd its inhibitory activity can be adjusted by mutation. Treatment
 CC with CD8 protein provides more selective immunosuppression than use of
 CC corticosteroids. The present sequence represents a cDNA encoding a human
 CC CD8 alpha protein
 XX
 SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,55e-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservativeness: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 2 Gaps: 1
 US-10-804-763-3 (1-198) x AAV80967 (1-708)
 QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 Db 1 ATGGCTTACCAAGTACCGCCCTTGTCTCCGCTGGCTTGTCTCCACGCCGCGAG 60
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 61 CCGAGCCAGTTCGGGTGTCGGCTGTGATCGAGCTGGAACTGGGGGAGACAGTGGAG 120
 QY 41 LeuLysCysGlnValLeuLeuSerHisProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 121 CTGAAGTGCAGGTGCTGTCTCCAAACCCGACGTGGGTGCTCTTCCAGCGC 180
 QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 181 CGCGGGCGCGCGCCAGTCCACCTTCTCTTATACCTTCTCCAAAACAGGCCAGGCG 240
 QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 241 GCGGAGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGACACCTTCGTCTC 300
 QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 301 ACCCTGAGCGACTTCGCGCGAGAACCGAGGGCTACTATTCTCGCGCCCTGAGCAAC 360
 QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 361 TCATCATGATGATTCAGGCACCTTCGTGCGGGTCTCTCTCCAGCGAGGCCACACGAGC 420
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 421 CCAGCGCGCGAGACCAACACCGCGCGCCACCATCGCGTCCAGCCCTGTCTCCCTGCGC 480
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 481 CCAGAGGGCGTGGCGGCCAGCGCGGGGGCGGAGTGCCACACGAGGGGGGTGGACTTCGCC 540

QY 171 ----- 171
 Db 541 TGTGATATCATCATCTGGGGCGCCCTTGGCGGGACTTGTGGGTCTCTTCTGTCTCACTG 600
 QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
 Db 601 GTTATCACCCCTTTACTTGCACACACAGAACCGAAGACGTGTTTGCAATGTCCCGCCT 660
 QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 661 GTGGTCAATCGGGAGACAAGCCCGCCCTTTCGGCGAGATACGTC 705

RESULT 6

ABZ69260

ID ABZ69260 standard; DNA; 708 BP.

XX AC ABZ69260;

XX DT 11-AUG-2003 (first entry)

XX DE Human CD8alpha chain coding sequence.

XX KW Human; CD8alpha; MHC binding; mutant; mutein; immunosuppressive;

XX KW antiallergic; cytotoxic T cell response; inhibitor; gene; ds.

XX OS Homo sapiens.

XX PN WO2002102852-A2.

XX PD 27-DEC-2002.

XX PF 14-JUN-2002; 2002WO-GB002743.

XX PR 14-JUN-2001; 2001GB-00014533.

XX PA (AVID-) AVIDEX LTD.

XX PI Jakobsen BK, Glick M;

XX DR WPI; 2003-167488/16.

XX DR P-PSDB; AAO19807.

XX New modified CD8 molecule having enhanced binding to major
 PT histocompatibility complex, and having a Serine53 of at least one CD
 PT alpha chain is mutated to another amino acid, useful for treating e.g.
 PT graft rejection or hypersensitivity.
 XX Disclosure; Fig 1A; 60pp; English.
 CC The present invention provides modified human CD8 molecules whose binding
 CC to major histocompatibility complex (MHC) is enhanced compared to wild
 CC type CD8. The modified CD8 molecule or a corresponding nucleic acid is
 CC useful in medicine, particularly in manufacturing a medicament for
 CC modulating CD8+ T cell response. The modified CD8 proteins and nucleic
 CC acids encoding such proteins are useful in immunosuppressive therapy,
 CC particularly as inhibitors of cytotoxic T cell responses, and for
 CC treating autoimmune disorders, hypersensitivity (e.g. allergic reaction),
 CC graft versus host disease, or graft rejection. The present sequence is a
 CC CD8 coding sequence

SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,55e-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservativeness: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 8 Gaps: 1

US-10-804-763-3 (1-198) x ABZ69260 (1-708)

```
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCTTTACAGTGCACCGCTTCTCTCGCGCTGGCTTGCCTCCACGCCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTATATCTCTCCCAAAACAAGCCCAAGCGG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTGTCTCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACCGAGGGCTACTATTTCTGCTGGGCTTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTTCAGCCACTTCTGTCGGCTTCTCTCCAGCGAAGCCACCGACG 420
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTGCAGCCCTGTCTCTGCGC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGGCGTGCAGCGCCAGCGCGCGCGCGCGAGTGCACACGAGGGGCTGAGCTTCGCC 540
Qy 171 ----- 171
Db 541 TGTGATATCTATCTGGCGCGCCCTTGGCCGGGACTTGTGGGCTCTTCTCTGTCTACTG 600
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCTTTACTGCAACACACAGGAAACCGAGACGTTGTTGCAATGTCCCGGCT 660
Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 661 GTGGTCAAAATCGGAGACAAGCCAGCCTTTTCGGCGAGATACGTC 705

RESULT 7
ADS92817
ID ADS92817 standard; cDNA; 708 BP.
XX
AC ADS92817;
XX
DT 16-DEC-2004 (first entry)
XX
DE Nucleotide sequence of a CD8 alpha-chain protein.
XX
KW immune response; cell-specific antigen; alloantigen; CD8;
KW CD8 alpha-chain; cellular immune response; humoral immune response;
KW transplant allograft; graft-versus-host disease; transplanted; gene; ss.
XX
OS Homo sapiens.
XX
PH Key
FT CDS
FT Location/Qualifiers
FT 1..708
FT /tag= b
FT /product= "CD8 alpha-chain"
FT sig_peptide
FT 1..63
FT /tag= a
XX
PN WO2004083244-A2.
XX
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```
PD 30-SEP-2004.
XX
PF 19-MAR-2004; 2004WO-US008574.
XX
PR 19-MAR-2003; 2003US-0456378P.
XX
PA (ISOG-) ISOGENIS INC.
XX
PI Qi Y, Zhang X, Konigsberg FJ;
XX
P-PSDB; ADS92816.
XX
DR WPI; 2004-691022/67.
XX
DR P-PSDB; ADS92816.
XX
XX Specifically inhibiting host immune responses to alloantigens, useful for
XX e.g. treating graft-versus-host disease, comprises contacting a target
XX cell expressing the antigen with an expression vector encoding a CD8
XX polypeptide.
XX
PS Disclosure; Fig 1; 98pp; English.
XX
XX The specification describes a method for specifically inhibiting a host
XX immune response to target cell-specific antigens (e.g. alloantigens). The
XX method comprises contacting a target cell expressing the antigen with an
XX expression vector encoding a CD8 polypeptide comprising the CD8 alpha-
XX chain, where the CD8 polypeptide is expressed by the target cell and
XX where the host immune response against the target cell is specifically
XX inhibited. The method of the invention is useful for specifically
XX inhibiting both cellular and humoral immune responses to alloantigens,
XX thus finding use in extending the survival of transplant allografts and
XX in treating graft-versus-host disease in transplant recipients. The
XX present sequence encodes the alpha-chain of a CD8 protein. This CD8 alpha
XX -chain may be used in the method of the invention.
XX
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-65 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 13 Gaps: 1

US-10-804-763-3 (1-198) x ADS92817 (1-708)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCTTTACAGTGCACCGCTTCTCTCGCGCTGGCTTGCCTCCACGCCGCCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 61 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTTGGGCGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGAGTCCACCTTCTCTATATCTCTCCCAAAACAAGCCCAAGCGG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGCAAGAGGTTGGGGACACCTTGTCTCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCCGCGGAGAGAACCGAGGGCTACTATTTCTGCTGGGCTTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTTCAGCCACTTCTGTCGGCTTCTCTCCAGCGAAGCCACCGACG 420
```

QY 141 ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 421 CCAGCCCGCGACCAACACCGCGCGCCACCATCGCTGCGAGCCCTGTCCCTGCGC 480
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 481 CCAGAGCGCTGCGGCGCAGCGCGGCGGCGGCGAGTCACACGAGGGGGTGGACTTCGCC 540
 QY 171 ----- 171
 Db 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTGTCTCACTG 600
 QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
 Db 601 GTTATCACCCTTTACTGCAACACACAGAACCGGAGACGTGTTTGCAAAATGTCCCCGGCCT 660
 QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 661 GTGGTCAAAATCGGAGACAGCCAGCCCTTTGGCGAGATACGTC 705

RESULT 8

ADSI19462

ID ADS19462 standard; DNA; 708 BP.

XX AC

XX ADS19462;

DT 16-DEC-2004 (first entry)

Coding sequence DNA of the human CD8 alpha chain mRNA.

gene; de; gene therapy; CD8 alpha chain; cellular immune response;

humoral immune response; immunosuppressive.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT 1..708

FT /*tag= a

FT /product= "CD8 alpha chain protein"

XX WO2004083404-A2.

XX PD 30-SEP-2004.

XX PF 19-MAR-2004; 2004WO-US008567.

XX PR 19-MAR-2003; 2003US-0456378P.

XX PA (ISOG-) ISOGENIS INC.

XX PI Qi Y, Zhang X, Konigsberg PJ;

XX WPI: 2004-691049/67.

XX DR P-PSDB; ADS19436.

PT New polynucleotide comprising a nucleic acid encoding a CD8 alpha-chain
 PT operably linked to a nucleic acid encoding a transmembrane polypeptide,
 PT useful for inhibiting cellular and humoral components of the host immune
 PT responses.

PS Disclosure; Fig 2a; 94pp; English.

XX This invention relates to novel gene therapy vectors with reduced
 CC immunogenicity. Specifically, it refers to a nucleic acid encoding a CD8
 CC alpha chain operably linked to nucleic acid encoding a transmembrane
 CC polypeptide and a second nucleic acid representing the therapeutic gene
 CC of interest (for example ornithine carbamoyl transferase or beta
 CC glucosidase), whereby transcriptional and translational control elements
 CC direct expression thereof. The present invention describes a method to
 CC reduce an immune response against antigens derived from a gene therapy
 CC delivery system i.e. improving the expression of a therapeutic transgene
 CC in a host and improving viral expression vectors with reduced
 CC immunogenicity. Accordingly, these compositions are useful for inhibiting

CC both the cellular and humoral components of the host immune responses
 CC against expression vectors and target cells transfected with the vectors.
 CC As such, they exhibit immunosuppressive activity, this polynucleotide is
 CC the coding sequence DNA of the human CD8 alpha chain mRNA of the
 CC invention.

XX SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,55e-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservatives: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 13 Gaps: 1

US-10-804-763-3 (1-198) x ADS19462 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
 Db 1 ATGGCCTTACCAGTACCGCCTTGTCTCGCGCTGGCCTTGTCTCCACGCGCCAGG 60
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 61 CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGGAGACAGTGGAG 120
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 121 CTGAAGTGCAGGTGCTGCTGCTCCAACCGCAGCTGGGGTGTCTGTGGTCTTCTCCAGCCG 180
 QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 181 CGCGCGCGCGCGCCAGTCCACCTTCTCTCTATACCTCTCCAAAAACAAGCCCAAGGCG 240
 QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 241 GCCGAGGGGTGGACACCCAGCGGTTCTGGGCGAGAGTTGGGGACACCTTCTGTCCTC 300
 QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 301 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTGGCCCTTGAGCAAC 360
 QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 361 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCCAGCGAAGCCACACGACG 420
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 421 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGCGTCGCGAGCCCTGTCTCCCTGCGC 480
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 481 CCAGAGGGGTGCCGCCAGCGCGGGGCGCGAGTCACACAGGGGGGTGGACTTCGCC 540
 QY 171 ----- 171
 Db 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGTCTCTCTGTCTCACTG 600
 QY 172 -----GlyAsnArgArgValCysLysCysProArgPro 183
 Db 601 GTTATCACCCTTTACTGCAACACACAGGAAACCGAAGACGTGTTTGCAAAATGTCCCCGGCCT 660
 QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 661 GTGGTCAAAATCGGAGACAGCCAGCCCTTTGGCGAGATACGTC 705

RESULT 9
 ADV42461
 ID ADV42461 standard; cDNA; 708 BP.
 XX AC ADV42461;
 XX DT 10-MAR-2005 (first entry)

XX DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 89.
XX KW microarray; psychoneuroendocrinimmune; chronic fatigue;
XX KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
XX KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX OS Homo sapiens.
XX FN WO2004108899-A2.
XX PD 16-DEC-2004.
XX FF 04-JUN-2004; 2004WO-US017696.
XX PR 04-JUN-2003; 2003US-0475915P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Nicholson A, Vernon SD;
XX DR WPI; 2005-031682/03.
XX KW New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX PS Claim 1; SEQ ID NO 89; 254pp; English.
XX CC The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
XX SEQ ID NO 1829 are provided.
SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,55e-65 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 14 Gaps: 1

US-10-804-763-3 (1-198) x ADV42461 (1-708)
Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCTTACAGTGACCGCTTGCTCTGCGCTGGCTTGCTGCTCCAGCCCGCAGG 60
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTCGGCTGGTGGACCTGGACCTGGCGGAGACAGTGGAG 120
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGAGCTGGGTGCTGCTGCTCTTCCAGCGG 180
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGG 240
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCCTC 300
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120

Db 301 ACCGTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 361 TCCATCATGTACTTACGCCACTTCGTGCGGTCTTCTGCGCGAGCAAGCCACACGACG 420
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGGACCAACACACCGGCGCCACCATCGCTCGCAGCCCTGTCCCTGCGC 480
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 481 CCAGAGCGGTGCCGCGCAGCGCGGGGGCGGCGCAGTGCACACGAGGGGCTGGACTTCGCC 540
Qy 171 ----- 171
Db 541 TGTGATATCTACATCTGCGGCGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCACTG 600
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 601 GTTATCACCCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCCCGGCT 660
Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 661 GTGGTCAAAATCGGAGACAGCCCGGCTTTCGGCGAGATACGTC 705

RESULT 10
AEF68357
ID AEF68357 standard; cDNA; 708 BP.
XX AC AEF68357;
XX DT 06-APR-2006 (first entry)
XX DE Human CD8 alpha chain cDNA.
XX KW immune inhibition; CD8; spinal cord injury; neuroprotective; vulnery;
KW autoimmune disease; immunosuppressive; immune disorder; diabetes;
KW antidiabetic; endocrine disease; gastrointestinal disease;
KW metabolic disorder; uveitis; antiinflammatory; ophthalmological;
KW inflammation; cirrhosis; hepatotropic; gastrointestinal disease;
KW neurodegenerative disease; neuroprotective; neurological disease;
KW osteoarthritis; antiarthritic; osteopathic; musculoskeletal disease;
KW obesity; anorectic; nutritional disorder; ss; gene.
XX OS Homo sapiens.
XX FH Location/Qualifiers
XX FT 1..708
XX FT /*tag= b
XX FT /product= "CD8 alpha chain"
XX FT /transl_except= (pos:67..69,aa:Gly)
XX FT /transl_except= (pos:130..132,aa:Gly)
XX FT /transl_except= (pos:175..177,aa:Gly)
XX FT /transl_except= (pos:223..225,aa:Gly)
XX FT /transl_except= (pos:259..261,aa:Gly)
XX FT /transl_except= (pos:463..465,aa:Gly)
XX FT 1..63
XX FT /*tag= a
XX FT mat_peptide 64..705
XX FT /*tag= c
XX FT /product= "Mature CD8 alpha chain"
XX FN WO2006012416-A2.
XX PD 02-FEB-2006.
XX PF 20-JUL-2005; 2005WO-US025878.
XX PR 20-JUL-2004; 2004US-0589707P.
XX PR 29-SEP-2004; 2004US-0614529P.
XX PA (ISOG-) ISOGENIS INC.

XX Q1 Y, Staerz UD;
 XX WPI; 2006-125925/13.
 DR P-PSDB; AEF68356.
 XX
 PT New composition comprising CD8 polypeptide and autoantigen protein,
 PT useful for preventing or treating autoimmune disease, diabetes,
 PT neurodegenerative diseases, osteoarthritis.
 XX
 PS Disclosure; Fig 1A; 85pp; English.
 XX
 CC The invention relates to a therapeutic composition for inhibiting an
 CC autoreactive T cell response, comprising an expression vector encoding a
 CC CD8 polypeptide and an autoantigen protein or its fragment, or at least
 CC one epitope of an autoantigen associated with the autoreactive T cell
 CC response. Also described are: (1) a polynucleotide comprising a first
 CC nucleic acid sequence encoding a CD8 polypeptide, a second nucleic acid
 CC sequence encoding at least one epitope of an autoantigen associated with
 CC an autoreactive T cell response, and control sequences operably linked
 CC with the first and second nucleic acids for expression in a target cell;
 CC (2) a method for inhibiting an autoimmune response to a target antigen;
 CC and (3) a method of preventing the development of or for treating an
 CC autoimmune disease in a host. The composition and methods are useful for
 CC inhibiting an autoimmune response to a target antigen, and for preventing
 CC the development of or for treating autoimmune disease, diabetes, uveitis,
 CC cirrhosis, neurodegenerative diseases (e.g. Alzheimer's disease,
 CC Huntington's disease, or Parkinson's disease), osteoarthritis, obesity,
 CC or spinal cord injury. The present sequence represents human CD8 alpha
 CC chain cDNA.
 XX
 SQ Sequence 708 BP; 119 A; 253 C; 207 G; 129 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,556-65 Length: 708
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservative: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 15 Gaps: 1

US-10-804-763-3 (1-198) x AEF68357 (1-708)

QY 1 MetaLaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 DB 1 ATGGCTTTACAGTACCGCTTGTCTCTGGCTGGCTTGTCTTCCAGCCGCGAG 60
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 DB 61 CCGAGCCAGTTCCGGGTGTCCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 120
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 DB 121 CTGAAGTCCAGGTGCTGCTGCCAACCGAGCTGGGCTGTCTGGTCTCTTCAGCGG 180
 QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 DB 181 CGGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAACAGGCCAAGGCG 240
 QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 DB 241 GCGGAGGGGCTGGACACCGCGGTTCGCGGCAAGAGGTTGGGGGACACCTTCGTCTC 300
 QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
 DB 301 ACCCTGAGCGACTCCGCGGAGAACGAGGGCTACTATTCTGTCTGGCGCTGAGCAAC 360
 QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 DB 361 TCCATCATGTACTTACGACACTTCTGGCGGTCTCTTCTGCCAGGAGCCACACGAGG 420
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

DB 421 CCAGCGCGCGGACACACACCGCGGCCACCATCGCGTTCGAGCCCTGTCTCCCTGGCG 480
 QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 DB 481 CCAGAGGCGGTGCTCGCGCCAGCGCGGCGCGAGTGTCACACAGAGGGGCTGGACTTCGCC 540
 QY 171 ----- 171
 DB 541 TGTGATATCTACATCTGGGCGCCCTTGGCGGAGACTTGTGGGGTCTCTCTCTGCTCACTG 600
 QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
 DB 601 GTTATCACCTTTACTGCAACACACAGGACCGAAGACGTGTTTGCAAATGTCCCGCCT 660
 QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaAlaTyrVal 198
 DB 661 GTGTCAATTCGGAGACAAAGCCACCTTCGGCGAGATACGTC 705

RESULT 11
 AAQ57986
 ID AAQ57986 standard; DNA; 1060 BP.
 AC AAQ57986;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-AUG-1994 (first entry)
 XX
 DE Genomic sequence of human CD8.
 XX
 KW gp39; T-cell antigen; CD40 ligand; B-cell proliferation; CD8;
 KW fusion protein; CD8; fusion protein; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 66..773
 FT /*tag= a
 XX
 PN EP585943-A2.
 XX
 PD 09-MAR-1994.
 XX
 PF 03-SEP-1993; 93EP-00114153.
 PR 04-SEP-1992; 92US-00940605.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Aruffo A, Hollenbaugh D, Ledbetter JA;
 XX
 DR WPI; 1994-076264/10.
 DR P-PSDB; AAR59550.
 XX
 PT New nucleic acid encoding human gp39 T cell antigen - which is a ligand
 PT for the CD40 receptor, causing proliferation and differentiation of B
 PT cells and some cancer cells.
 XX
 PS Disclosure; Fig 9; 39pp; English.
 XX
 CC The complete nucleic acid sequence of human gp39 (hgp39) protein
 CC (corresp. to cDNA) and the complete AA sequence of hgp39 are presented in
 CC AAQ57984 and AAR49548 respectively and contd. in plasmid CDM8-hgp39,
 CC deposited with the ATCC as E. coli, CDM8 MC1061/p3-hgp39 and assigned
 CC accession No. 69050. The human T cell antigen gp39 is a ligand for the
 CC CD40 receptor. Soluble gp39 may be produced using the expression vector
 CC CDM8-gp39. Chimeric genes may be constructed by fusing sequences encoding
 CC the extracellular domains of gp39 and CD8, pref. murine or human CD8
 CC protein, plasmid p3-shgp39 encoding the fusion protein of the
 CC extracellular domains from gp39 and CD8 is deposited in E.coli as ATCC
 CC 69049. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

| | | | | | | | | | |
|---|---|--|------|--|--|--|--|--|--|
| Alignment Scores: | | | | | | | | | |
| Pred. No.: | 4.02e-65 | Length: | 1060 | | | | | | |
| Score: | 1006.50 | Matches: | 197 | | | | | | |
| Percent Similarity: | 83.8% | Conservative: | 0 | | | | | | |
| Best Local Similarity: | 83.8% | Mismatches: | 1 | | | | | | |
| Query Match: | 96.5% | Indels: | 37 | | | | | | |
| DB: | 2 | Gaps: | 1 | | | | | | |
| US-10-804-763-3 (1-198) x AAQ57986 (1-1060) | | | | | | | | | |
| QY | 1 | MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiaAlaAaArg | 20 | | | | | | |
| DB | 66 | ATGCGCTTACAGTACAGCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCGCAGG | 125 | | | | | | |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 | | | | | | |
| DB | 126 | CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG | 185 | | | | | | |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 | | | | | | |
| DB | 186 | CTGAAGTGCCAGGTGCTGCTTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCCAGCG | 245 | | | | | | |
| QY | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 | | | | | | |
| DB | 246 | CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTTCTCCAAAACAAGCCCAAGGCG | 305 | | | | | | |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 | | | | | | |
| DB | 306 | CCCGAGGGCTGGACACCGAGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTC | 365 | | | | | | |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn | 120 | | | | | | |
| DB | 366 | ACCTTGAGCGACTTCGCGCGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCAAC | 425 | | | | | | |
| QY | 121 | SerIleuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 | | | | | | |
| DB | 426 | TCCATCATGTACTTCAGCCACTTCTGTCGCGGTCTTCTCGCAGCGAAGCCACACGAGC | 485 | | | | | | |
| QY | 141 | ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 | | | | | | |
| DB | 486 | CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCCCTGTCTCTGCGC | 545 | | | | | | |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAla | 171 | | | | | | |
| DB | 546 | CCAGAGCGGTGCGCGCACCGCGCGCGCGCGCAGTCACACAGCGGGCTGGACTTCGCC | 605 | | | | | | |
| QY | 171 | | 171 | | | | | | |
| DB | 606 | TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGCTCACTG | 665 | | | | | | |
| QY | 172 | | 172 | | | | | | |
| DB | 666 | GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAATGTCCTCCCGGCT | 725 | | | | | | |
| QY | 184 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 198 | | | | | | |
| DB | 726 | GTGGTCAAAATCGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTC | 770 | | | | | | |
| RESULT 12 | | | | | | | | | |
| ADD25612 | | | | | | | | | |
| ID | ADD25612 standard; DNA; 1060 BP. | | | | | | | | |
| XX | | | | | | | | | |
| AC | | | | | | | | | |
| XX | | | | | | | | | |
| DT | 15-JAN-2004 (first entry) | | | | | | | | |
| XX | | | | | | | | | |
| DE | Binding domain-immunoglobulin fusion protein-associated DNA #90. | | | | | | | | |
| XX | | | | | | | | | |
| KW | ds; Binding domain; immunoglobulin; fusion protein; cytostatic; | | | | | | | | |
| KW | antiarthritic; immunosuppressive; antidiabetic; antithyroid; | | | | | | | | |
| KW | neuroprotective; hinge region; immunoglobulin heavy chain; | | | | | | | | |
| KW | CH2 constant region; CH3 constant region; IgG1; | | | | | | | | |
| KW | antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; | | | | | | | | |

| | | | |
|---|---|--|-----|
| KW | malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; | | |
| KW | rheumatoid arthritis; myasthenia gravis; Grave's disease; | | |
| XX | type I diabetes mellitus; multiple sclerosis; autoimmune disease. | | |
| OS | Unidentified. | | |
| XX | | | |
| PN | US2003118592-A1. | | |
| XX | | | |
| PD | 26-JUN-2003. | | |
| XX | | | |
| PF | 25-JUL-2002; 2002US-00207655. | | |
| XX | | | |
| PR | 17-JAN-2001; 2001US-0367358P. | | |
| PR | 17-JAN-2002; 2002US-00053530. | | |
| PR | 03-JUN-2002; 2002US-0385691P. | | |
| XX | | | |
| PA | (GENE-) GENE-CRAFT INC. | | |
| XX | | | |
| PI | Ledbetter JA, Hayden-Ledbetter MS, Thompson PA; | | |
| XX | | | |
| DR | WPI; 2003-801317/75. | | |
| XX | | | |
| PT | New binding domain-immunoglobulin fusion protein, useful for treating a | | |
| PT | subject having or suspected of having a malignant condition or a B-cell | | |
| PT | disorder, e.g. melanoma, Grave's disease or autoimmune disease. | | |
| XX | | | |
| PS | Disclosure; SEQ ID NO 173; 157pp; English. | | |
| XX | | | |
| CC | Unidentified | | |
| XX | | | |
| SQ | Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other; | | |
| Alignment Scores: | | | |
| Pred. No.: | 4.02e-65 | | |
| Score: | 1006.50 | | |
| Percent Similarity: | 83.8% | | |
| Best Local Similarity: | 83.8% | | |
| Query Match: | 96.5% | | |
| DB: | 10 | | |
| Gaps: 1 | | | |
| US-10-804-763-3 (1-198) x ADD25612 (1-1060) | | | |
| QY | 1 | MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHiaAlaAaArg | 20 |
| DB | 66 | ATGCGCTTACAGTACAGCGCTTGTCTCTCGCGCTGGCTTGTCTCCAGCGCGCAGG | 125 |
| QY | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| DB | 126 | CCGAGCCAGTTCGGGTGTCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG | 185 |
| QY | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| DB | 186 | CTGAAGTGCCAGGTGCTGCTGTCCAAACCGACGTCGGGCTGCTGTGGCTCTTCCAGCGC | 245 |
| QY | 61 | ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
| DB | 246 | CGCGCGCGCGCGCGAGTCCACCTTCTCTATACCTTCTCCAAAACAAGCCCAAGGCG | 305 |
| QY | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
| DB | 306 | CCCGAGGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTC | 365 |
| QY | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn | 120 |
| DB | 366 | ACCTTGAGCGACTTCGCGCGAGAGACGAGGCTACTATTCTGCTCGGCCCTGAGCAAC | 425 |
| QY | 121 | SerIleuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 |
| DB | 426 | TCCATCATGTACTTCAGCCACTTCTGTCGCGGTCTTCTCGCAGCGAAGCCACACGAGC | 485 |
| QY | 141 | ProAlaProArgProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| DB | 486 | CCAGCGCGCGACCAACACCGCGCGCCACCATCGCGTCGAGCCCTGTCTCTGCGC | 545 |
| QY | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAla | 171 |
| DB | 546 | CCAGAGCGGTGCGCGCACCGCGCGCGCGCGCAGTCACACAGCGGGCTGGACTTCGCC | 605 |
| QY | 171 | | 171 |
| DB | 606 | TGTGATATCTACATCTGGGCGCCCTTGGCGGGGACTTGTGGGTCTCTCTCTGCTCACTG | 665 |
| QY | 172 | | 172 |
| DB | 666 | GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAATGTCCTCCCGGCT | 725 |
| QY | 184 | ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 198 |
| DB | 726 | GTGGTCAAAATCGGAGACAAGCCAGCCCTTTTCGGCGAGATACGTC | 770 |
| RESULT 12 | | | |
| ADD25612 | | | |
| ID | ADD25612 standard; DNA; 1060 BP. | | |
| XX | | | |
| AC | | | |
| XX | | | |
| DT | 15-JAN-2004 (first entry) | | |
| XX | | | |
| DE | Binding domain-immunoglobulin fusion protein-associated DNA #90. | | |
| XX | | | |
| KW | ds; Binding domain; immunoglobulin; fusion protein; cytostatic; | | |
| KW | antiarthritic; immunosuppressive; antidiabetic; antithyroid; | | |
| KW | neuroprotective; hinge region; immunoglobulin heavy chain; | | |
| KW | CH2 constant region; CH3 constant region; IgG1; | | |
| KW | antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; | | |

QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Dbb 546 CCAGAGCGTGCCTCGCGCAGCGCGGGGGCGCAGTGACACAGAGGGGGTGGACTTCGGC 605
QY 171 ----- 171
Db 606 TGTGATATCTACATCTGGCGCGCTTGGCGGAGCTTGGGGTCTCTCTCTGTGACATG 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCTTTACTGCAACACACAGGACCGAGACGTGTTGGAAATGTCCTCGGCT 725
QY 184 ValVallYsSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 726 GTGGTCAATCGGGAGACAAAGCCAGCTTTCCGGCGAGATACGTC 770

RESULT 13

AD131688

ID AD131688 standard; cDNA; 1060 BP.

XX

AC AD131688;

XX

DT 17-JUN-2004 (first entry)

XX

DE Human cDNA #1014.

XX

KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersensitivity; irritable
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiaesthmic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX

OS Homo sapiens.

XX

FN US6607879-B1.

XX

PD 19-AUG-2003.

XX

PF 09-FEB-1998; 98US-00023655.

XX

PR 09-FEB-1998; 98US-00023655.

XX

PA (INCY-) INCYTE CORP.

XX

Cocks BG, Stuart SG, Seilhamer JJ;

XX

WPI; 2003-895307/82.

XX

PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

XX

PS Claim 1; SEQ ID NO 1014; 50pp; English.

XX

CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,

CC ulcerative colitis, hypersensitivity, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX

SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4, 02e-65 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 11 Gaps: 1

US-10-804-763-3 (1-198) x AD131688 (1-1060)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Dbb 66 ATGGCTTACCAGTACCGCTTGTCTCTCGCTGGCTTGTCTCCACGCGCCAGG 125
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGlnThrValGlu 40
Dbb 126 CCGAGCCAGTTCCTGGGTGCGCGCTGGATCGGACTGGAACTGGGGCAGACAGTGGAG 185
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Dbb 186 CTGAAGTCCAGGTCTGTCTCCAAACCCGACGTGGGCTGTCTGTGGCTCTTCCAGCCG 245
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Dbb 246 CGCGCGCGCGCGCGCGCTCCACCTTCTCTATACCTCTCCAAACAGGCGCAAGGCG 305
QY 81 AlaGlyLeuLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Dbb 306 CGCGAGGGGGTGGACACCGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 365
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Dbb 366 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTCTCGGCCCTGAGCAAC 425
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Dbb 426 TCCATCATGTACTTCAGGCACCTTCGTGGCGGTCTTCTGCCAGCGAAGCCACCGACG 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Dbb 486 CCAGCGCGCGACCAACCAACCGCGCGCCACCATCGGTGCGACCCCTGTCTCTCTGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Dbb 546 CCAGAGGGGTGCGCGCGCAGCGCGGGGGCGCGCAGTGCAACAGAGGGGGCTGAGCTTCGCC 605
QY 171 ----- 171
Dbb 606 TGTGATATCTATACATCTGGCGCGCTTGGCGGAGCTTGTGGGGTCTTCTCTCTGTCTC 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Dbb 666 GTTATCACCTTTACTGCAACACACAGGAAACCGAAGACGTGTTGGAAATGTCCTCGGCT 725
QY 184 ValVallYsSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Dbb 726 GTGGTCAATCGGGAGACACCGCCAGCTTTCCGGCGAGATACGTC 770

RESULT 14

ADS83755

ID ADS83755 standard; cDNA; 1060 BP.
 AC ADS83755;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Human lymph node cDNA #1014.
 XX
 KW ss; gene; human; immunological response; blood cell; cancer;
 KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
 KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
 KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
 XX
 OS Homo sapiens.
 XX
 FN US2004077003-A1.
 XX
 XX 22-APR-2004.
 XX
 XX 14-AUG-2003; 2003US-00641643.
 XX
 XX 09-FEB-1998; 98US-00023655.
 XX
 XX (INCY-) INCYTE CORP.
 XX
 XX Cocks BG, Stuart SG, Seilhamer JJ;
 XX
 XX WPI; 2004-387937/36.
 XX
 XX New compositions having a number of first, second and third
 PT polynucleotide probes, useful in research and diagnostic applications in
 PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
 PT infections.
 XX
 XX Claim 15; SEQ ID NO 1014; 16pp; English.
 XX
 CC The invention relates to polynucleotides which are used as probes to
 CC detect genes differentially expressed in an immunological response,
 CC abundantly expressed in an immunological response and/or coding for a
 CC polypeptide known to regulate blood cell biology. The polynucleotides are
 CC useful in research and diagnostic applications particularly in cancer and
 CC immunopathological conditions, such as AIDS, allergies, asthma,
 CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
 CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
 CC present sequence represents a human lymph node cDNA used to detect blood
 CC cell and immunological response gene expression. Note: The present
 CC sequence does not appear in the printed specification but was obtained in
 CC electronic format from the USPTO web site
 CC (ssqdata.uspto.gov/sequence.html?docID=20040077003).
 XX
 SQ Sequence 1060 BP; 196 A; 349 C; 294 G; 221 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 4, 02e-65 Length: 1060
 Score: 1006.50 Matches: 197
 Percent Similarity: 83.8% Conservative: 0
 Best Local Similarity: 83.8% Mismatches: 1
 Query Match: 96.5% Indels: 37
 DB: 13 Gaps: 1
 US-10-804-763-3 (1-198) x ADS83755 (1-1060)
 Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
 Db 66 ATGGCCCTTACAGTACCGCTTCTGCTCGCGTGGCTTGTCTCCAGCCGCGCAGG 125
 Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
 Db 126 CCGAGCCAGTTCGGGGTTCGGCGTGGATCGGACCTGGAAACCTGGGGGAGACATGGAG 185
 Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 Db 186 CTGAAGTCCAGGCTGCTGTGCCAACCCGAGCTCGGGCTGCTCGTGGCTCTTCCAGCGG 245

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
 Db 246 CGCGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCAAAACAAGCCCAAGCGC 305
 Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 Db 306 GCCGAGGGGCTGGACACCCAGCGGTTCTGGGCAAGAGGTTGGGGGACACCTTCTCTC 365
 Qy 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
 Db 366 ACCCTGAGCGACTTCCCGCGAGAGACAGAGGCTACTATTCTCTGCTGGCCCTGAGCAAC 425
 Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 Db 426 TCCATCATGTACTTTCAGCCACTTCTGCGCGGCTTCTCTGCCAGCGAAGCCCAACGACG 485
 Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 Db 486 CCAGCGCGCGACCCACCAACACCGCGGCCACCATCGGTCGCGAGCCCTGTCTCTGCGC 545
 Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
 Db 546 CCAGAGGCGTCCGCGCCAGCGCGGGGGCGCAGTGCACACAGGGGGCTGGACTTCGCC 605
 Qy 171 ----- 171
 Db 606 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCTGCACTG 665
 Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
 Db 666 GTTATACCCCTTTACTGCACACAGGACCGAAGACGTGTTGCAATGTCCCCGGGCT 725
 Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 Db 726 GTGTGCAATCGGAGACACAGCCCGCCCTTTCGGGCGAGATACGTC 770
 RESULT 15
 ADF90782
 ID ADF90782 standard; DNA; 2123 BP.
 AC ADF90782;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Human hepatic-fibrosis disease marker SEQ ID 244.
 XX
 KW Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 KW hepatic carcinoma; human; ds.
 XX
 OS Homo sapiens.
 XX
 XX JP2003259877-A.
 XX
 PD 16-SEP-2003.
 XX
 PF 11-MAR-2002; 2002JP-00065013.
 XX
 PR 11-MAR-2002; 2002JP-00065013.
 XX
 XX (SUMU) SUMITOMO SEIYAKU KK.
 XX
 XX WPI; 2003-821598/77.
 XX
 PT Hepatic fibrosis disease markers comprising polynucleotides or
 PT antibodies, useful for improved diagnosis, screening and developing drugs
 PT to treat hepatitis, to control cirrhosis and carcinoma.
 XX
 PS Claim 1; SEQ ID NO 244; 313pp; Japanese.
 XX
 CC The present invention relates to hepatic-fibrosis disease markers
 CC (ADF90539-ADF90871) and related proteins (ADF90872-ADF90917). The
 CC sequences are useful for detecting and treating hepatic fibrosis caused

CC by alcohol consumption, virus infection, etc., and the associated chronic
CC hepatitis, etc. leading to liver cirrhosis and hepatic carcinoma. The
CC markers allow the cause of hepatic fibrosis to be clarified (diagnostic
precision), so more suitable treatments can be developed and given.
XX

SQ Sequence 2123 BP; 508 A; 586 C; 528 G; 501 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
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US-10-804-763-3 (1-198) x ADF90782 (1-2123)

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| Db | 141 | CCGAGCCAGTTCGGGGTGTGCGCGTGGATCGGACCTGGAACTGGGCGGAGACAGTGGAG | 200 |
| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 201 | CTGAAGTGCAGGTGCTGTCTCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCCG | 260 |
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| Qy | 101 | ThrLeuSerAspPheArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn | 120 |
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Job time : 768.277 secs

GenCore version 5.1.8
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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 1006.5 | 96.5 | 1060 | 3 | US-09-023-655-1014 Sequence 1014, Ap |
| 4 | 997.5 | 95.6 | 2150 | 5 | US-10-131-831-9109 Sequence 9109, Ap |
| 5 | 899 | 86.2 | 1131 | 3 | US-08-751-512-7 Sequence 7, Appl |
| 6 | 623 | 59.7 | 822 | 2 | US-08-403-853-11 Sequence 11, Appl |
| 7 | 352.5 | 33.8 | 803 | 3 | US-09-477-737-2 Sequence 2, Appl |
| 8 | 352.5 | 33.8 | 972 | 2 | US-07-940-605A-9 Sequence 9, Appl |

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| 10 | 311 | 29.8 | 8345 | 3 | US-09-966-976A-8 | Sequence 8, Appl |
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| 16 | 135 | 12.9 | 1202 | 2 | US-08-491-988-27 | Sequence 27, Appl |
| 17 | 132 | 12.7 | 1178 | 2 | US-08-491-988-28 | Sequence 28, Appl |
| 18 | 132 | 12.7 | 1235 | 2 | US-08-491-988-11 | Sequence 11, Appl |
| 19 | 131.5 | 12.6 | 1259 | 3 | US-08-491-988-24 | Sequence 24, Appl |
| 20 | 129 | 12.4 | 315 | 3 | US-10-083-424-31 | Sequence 31, Appl |
| 21 | 128.5 | 12.3 | 927 | 2 | US-07-690-192-1 | Sequence 1, Appl |
| 22 | 127.5 | 12.2 | 1295 | 2 | US-08-491-988-26 | Sequence 26, Appl |
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| 24 | 127 | 12.2 | 1178 | 2 | US-08-491-988-25 | Sequence 25, Appl |
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| 26 | 125 | 12.0 | 805 | 3 | US-09-620-312D-62 | Sequence 62, Appl |
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| 31 | 124.5 | 11.9 | 431 | 2 | US-08-345-321-7 | Sequence 3743, Ap |
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| 41 | 123 | 11.8 | 938 | 3 | US-09-828-995B-25 | Sequence 27, Appl |
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ALIGNMENTS

RESULT 1
US-07-940-605A-11
; Sequence 11, Application US/07940605A
; Patent No. 5540926
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090

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; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-940-605A-11

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Pred. No.: 3.14e-76 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTCGCGCTGGATCGGACCTGGAACCTGGGCGAGACAGTGGAG 185

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; Patent No. 5945513
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; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,096
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/940,605
; FILING DATE: 04-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-3090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-690-096-11

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Pred. No.: 3.14e-76 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x US-08-690-096-11 (1-1060)

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Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
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; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
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; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

; CLONE: g179145
; US-09-023-655-1014
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Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservatives: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
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QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCCCTTTACTGCAACCAACGAGAACCGAAGACGTGTTTGCAAAATGTCCCGGCT 725
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
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; Sequence 9109, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121

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; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9109
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-9109

Alignment Scores:
Pred. No.: 4,56e-75 Length: 2150
Score: 997.50 Matches: 196
Percent Similarity: 83.4% Conservative: 0
Best Local Similarity: 83.4% Mismatches: 2
Query Match: 95.6% Indels: 37
DB: 5 Gaps: 1

US-10-804-763-3 (1-198) x US-10-131-831-9109 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 6 ATGGCCCTTACCAGTGACCGCTTGCTCGCGCTGGCTTGCTGCCCGCCGAGG 65

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 66 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 125

Qy 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 126 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGTGCTCGTGGCTCTTCAGCGC 185

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 186 CGCGCGCGCGCGCGCGCGCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGC 245

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 246 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAGAGAGTGGGGGACACCTTCGTCTC 305

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 306 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTGCTATTTCTGCTCGGCTGAGCAAC 365

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 366 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCCTGCCAGCGAAGCCACCAAGCG 425

Qy 141 ProAlaProAspProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 426 CCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 485

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 486 CCAGAGGGCGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545

Qy 171 ----- 171
Db 546 TGTGATATCTAATCTGGCGCGCGCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 605

Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 606 GTTATCACCTTTACTGCAACACAGAGAACCGAAGACGTGTTTGCATATGCTCCCGGCT 665

Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 666 GTGGTCAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 710

US-08-751-512-7
; Sequence 7, Application US/08751512
; Patent No. 6001962
; GENERAL INFORMATION:
; APPLICANT: Ramer, J. Kevin
; APPLICANT: Williams, Lewis T.
; TITLE OF INVENTION: Modified FAS Ligands
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,512
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Matthew B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 02307K-07100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1131 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1128
US-08-751-512-7

Alignment Scores:
Pred. No.: 4.31e-67 Length: 1131
Score: 899.00 Matches: 172
Percent Similarity: 98.9% Conservative: 1
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 86.2% Indels: 0
DB: 3 Gaps: 0

US-10-804-763-3 (1-198) x US-08-751-512-7 (1-1131)

Qy 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGGCCCTTACCAGTGACCGCTTGCTCGCGCTGGCTTGCTGCCCGCCGAGG 60

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 CCGAGCCAGTTCGGGTGTCGGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120

Qy 41 LeuIysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 121 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGGTGCTCGTGGCTCTTTCAGCGC 180

Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 181 CGCGCGCGCGCGCGCGCGCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGC 240

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 241 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAGAGAGTGGGGGACACCTTCGTCTC 300

RESULT 5
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QY 101 ThrLeuSerAspPheArgGluAenGluGlyTyrTyPheCysSerAlaLeuSerAsn 120
Db 301 ACCCTGAGCGACTTCGCGCAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 360
QY 121 SerIleMetTyPheSerHisPheValProValPheLeuProAlaLysP-othrThrThr 140
Db 361 TCATCATGTACTTCAGCCACATTCGTGCGCGGTCTTCTGCTCCAGCAAGCCACCAGCG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 421 CCAGCGCGCGACCCACCAACACCGCGGCCACCATCGCTGCGAGCCCTGTCTCCCTGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArg 175
Db 481 CCAGAGGCGTGGCGCGCAGCGCGGGGGGGCGGCGAGTGCACACGAGG 525

RESULT 6

US-08-403-853-11
; Sequence 11, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/AU93/00491
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PL 4973
; FILING DATE: 25-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16786/189/CHAC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 822 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..819
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..819

US-08-403-853-11

Alignment Scores:
Pred. No.: 6,6e-44 Length: 822
Score: 623.00 Matches: 124
Percent Similarity: 94.0% Conservative: 1
Best Local Similarity: 93.2% Mismatches: 2
Query Match: 59.7% Indels: 6
DB: 2 Gaps: 2

US-10-804-763-3 (1-198) x US-08-403-853-11 (1-822)

QY 9 LeuLeuProLeuAla-----LeuLeuLeuHisAlaAlaArgPro-----Ser 22
Db 10 CTATTGCCTACGCGCAGCGCTGGATTGTTATTACTGCTGCTGCCAACACCGATGGCCAGC 69
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 70 CAGTTCCGGGTGTCGCGCTGGATCGGACCTCGGAACCTGGCGGAGACAGTGGAGCTGAAG 129
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrLeuPheGlnProArgGly 62
Db 130 TGCCAGGTGCTGCTGTCTCCAACCCGAGCTCGGGCTGCTGCTGCTCTTCCAGCGCGCGGC 189
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 190 GCGGCGCGCAGTCCACCTTCTCTATACCTCTCCAAAAACAAGCCCAAGCGCGCGAG 249
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 250 GGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCCTCCTCACCCCTG 309
QY 103 SerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db 310 AGCGACTTCCCGCGAGAGAACGAGGCTACTATTCTGCTGCGCCCTGAGCAACTCCATC 369
QY 123 MetTyrPheSerHisPheValProValPheLeuProAla 135
Db 370 ATGTACTTCAGCCACTTCGTGCGCGGTCTTCTGCGCAGCG 408

RESULT 7

US-09-477-737-2
; Sequence 2, Application US/09477737
; Patent No. 6544506
; GENERAL INFORMATION:
; APPLICANT: Reischer
; TITLE OF INVENTION: VETO CELLS EFFECTIVE IN PREVENTING GRAFT REJECTION AND DEVOID O.
; FILE OF INVENTION: VERSUS HOST POTENTIAL
; FILE REFERENCE: 00/20548
; CURRENT APPLICATION NUMBER: US/09/477,737
; CURRENT FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-477-737-2

Alignment Scores:
Pred. No.: 5,08e-21 Length: 803
Score: 352.50 Matches: 96
Percent Similarity: 51.6% Conservative: 33
Best Local Similarity: 38.4% Mismatches: 66
Query Match: 33.8% Indels: 55
DB: 3 Gaps: 13

US-10-804-763-3 (1-198) x US-09-477-737-2 (1-803)

QY .1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14
Db 13 ATGGCCCTCACCGTTGACCGCGCTTCTGCTGCTGAACCTGCTGCTGCTGGTGAGTCGATT 72

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Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 73 ATCTGGGGAGTGGAGAACTAAAGCCACAGCCAGCACTCCGAATCTTCCAAAGAAA 132
Qy 31 ArgThrTrpAenLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 133 ATGACGCCAGCACTTGGTCAGAAAGTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 189
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 190 TCGCAAGAGTACTCTTGGCTCTTCAGAACTCCAGCTCCAACTCCCCAGCCACCTTC 249
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 250 GTTGCTATATGGCTTCTATCCCAACAAGATAACGTGGGACGAGAAGCTGAATTCGTCG 309
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 310 AAACCTGTTTCTGCCATGAGGACGACGAAATAATAGTACGTTCTCACCTGAAACAGTTC 369
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 370 AGCAAGGAAAACGAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 429
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
Db 430 AGTTCTGTGCGCCAGTCTTCAGAAAGTGAACTCTACTACTACCAAGCCAGTGTGCGA 489
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 490 ACTCCCTCACCCTGTCACCTACCGGACATCTCAGCCC-----CAGAGACCAAGAT 543
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGly----- 172
Db 544 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGATTGGACTTCGCTGTGATATTTACATC 603
Qy 172 ----- 172
Db 604 TGGGACCCCTTGGCGGAAATCTGGTGCCCTTCTGCTGCTGTGATCATCTCTCATC 663
Qy 173 ----- 173
Db 664 TGCTACCACAGGACCGGAAGGGTGTGGCAATGTCCAGGCCCTAGTCAGACAGGAA 723
Qy 189 AspLysProSerLeuSerAlaArgTyrVal 198
Db 724 GGCAAGCCAGACCTTTCAGAGAAAATTGTG 753
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RESULT 8

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US-07-940-605A-9
; Sequence 9, Application US/07940605A
; Patent No. 5540926
;
; GENERAL INFORMATION:
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: HOLLENBAUGH, DIANE
; APPLICANT: LEDBETTER, JEFFREY A.
; TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,605A
; FILING DATE: 04-SEP-1992
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; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-07-940-605A-9
;
; Alignment Scores:
; Pred. No.: 6.51e-21 Length: 972
; Score: 352.50 Matches: 96
; Percent Similarity: 51.6% Conservative: 33
; Best Local Similarity: 38.4% Mismatches: 66
; Query Match: 33.8% Indels: 55
; DB: 2 Gaps: 13
;
; US-10-804-763-3 (1-198) x US-07-940-605A-9 (1-972)
;
; Qy 1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14
; Db 127 ATGCGCTCACCGTTGACCGCTTCTGTCGCTGAACCTGCTGCTGGTGAGTCGATT 186
;
; Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
; Db 187 ATCTGGGGAGTGGAGAACTAAAGCCACAGGACCCGAACTCCGAATCTTCCAAAGAAA 246
;
; Qy 31 ArgThrTrpAenLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
; Db 247 ATGACGCCAGCACTTGGTCAGAAAGTGACCTGGTATGTGAAGTG---TTGGGGTCCGTT 303
;
; Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
; Db 304 TCGCAAGAGTCTCTTGGCTCTTCAGAACTCCAGCTCCAACTCCCCAGCCACCTTC 363
;
; Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
; Db 364 GTTGCTATATGGCTTCTATCCCAACAAGATAACGTGGGACGAGAAGCTGAATTCGTCG 423
;
; Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
; Db 424 AAACCTGTTTCTGCCATGAGGACACGAAATAATAGTACGTTCTCACCTGAAACAGTTC 483
;
; Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
; Db 484 AGCAAGGAAAACGAAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 543
;
; Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThrThr---ProAlaProArg 144
; Db 544 AGTTCTGTGCGCCAGTCTTTCAGAAAGTGAACTCTACTACTACCAAGCCAGTGTGCGA 603
;
; Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
; Db 604 ACTCCCTCACCCTGTCACCTACCGGACATCTCAGCCC-----CAGAGACCAAGAT 657
;
; Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGly----- 172
; Db 658 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGATTGGACTTCGCTGTGATATTTACATC 717
;
; Qy 172 ----- 172
; Db 718 TGGGACCCCTTGGCGGAAATCTGGTGCCCTTCTGCTGCTGTGATCATCTCTCATC 777
;
; Qy 173 ----- 173
; Db 173 ----- 173
; Qy 173 ----- 173
; Db 173 ----- 173
; Qy 173 ----- 173
; Db 173 ----- 173
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Query Match: 29.8% Indels: 22
DB: 3 Gaps: 12

US-10-804-763-3 (1-198) x US-09-966-976A-8 (1-8345)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14
Db 4974 ATGCGCTCACCGTTGACCGCGTTTCTGTCGTGAACCTGCTGCTGGTGAGTCGATT 4915
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 4914 ATCTGGGGAGTGGAGAGCTAAGCCACAGCAGCCCGAACTCCGAATCTTTCCAAAGAAA 4855
Qy 31 ArgThrTrpAsnLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 4854 ATGACGCCGGAACCTTGGTCAGAGGAGCTGGTATGTGAAGTG---TTGGGGTCCGTT 4798
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 4797 TCGCAAGGATGCTCTTGGCTCTCCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 4738
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 4737 GTTGTCTATATGCTTCTATCCACACAAAGATAACGTGGGACGAGAACTGAATTCGTCG 4678
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 4677 AAACCTGTTTCTGCCATGAGGACACGAAATAAATAGTACGTTCTCACCTGAACAAGTTC 4618
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 4617 AGCAAGGAAACGAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 4558
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThr---ProAlaProArg 144
Db 4557 AGTTCTGTCGTGCGCAGCTCTTTCAGAAAGTGAACCTACTACTACCAAGCCAGTGTGCGA 4498
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 4497 ACTCCCTCACCTGTGCACCTACCGGACATCTCAGCCC-----CAGAGACCAGAAGAT 4444
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGlyAsnArg 174
Db 4443 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGAACCGG 4405

RESULT 11
US-09-076-624-8/c
; Sequence 8, Application US/09076624A
; Patent No. 7001733
; GENERAL INFORMATION:
; APPLICANT: FERRICK et al.
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators
; TITLE OF INVENTION: and Ige Synthesis, Secretion and Switch Rearrangement
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/076,624A
; CURRENT FILING DATE: 1998-05-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-076-624-8

Alignment Scores:
Pred. No.: 3.48e-16 Length: 8345
Score: 311.00 Matches: 84
Percent Similarity: 58.0% Conservativeness: 28
Best Local Similarity: 43.5% Mismatches: 59
Query Match: 29.8% Indels: 22
DB: 5 Gaps: 12

US-10-804-763-3 (1-198) x US-09-076-624-8 (1-8345)

Qy 1 MetAlaLeuProValThr-----AlaLeuLeuLeuProLeuAlaLeu 14
Db 4974 ATGCGCTCACCGTTGACCGCGTTTCTGTCGTGAACCTGCTGCTGGTGAGTCGATT 4915
Qy 15 LeuLeuHisAla-----AlaArgProSer-----GlnPheArgValSerProLeuAsp 30
Db 4914 ATCTGGGGAGTGGAGAGCTAAGCCACAGCAGCCCGAACTCCGAATCTTTCCAAAGAAA 4855
Qy 31 ArgThrTrpAsnLeuGluThrValGluLeuLysCysGlnValLeuLeuSerAsnPro 50
Db 4854 ATGACGCCGGAACCTTGGTCAGAGGAGCTGGTATGTGAAGTG---TTGGGGTCCGTT 4798
Qy 51 ThrSerGlyCysSerTrpLeuPheGlnProArgGlyAla---AlaAlaSerProThrPhe 69
Db 4797 TCGCAAGGATGCTCTTGGCTCTCCAGAACTCCAGCTCCAAACTCCCCACCCACCTTC 4738
Qy 70 LeuLeuTyrLeu-----SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGln 87
Db 4737 GTTGTCTATATGCTTCTATCCACACAAAGATAACGTGGGACGAGAACTGAATTCGTCG 4678
Qy 88 Arg---PheSerGlyLysArg---LeuGlyAspThrPheValLeuThrLeuSerAspPhe 105
Db 4677 AAACCTGTTTCTGCCATGAGGACACGAAATAAATAGTACGTTCTCACCTGAACAAGTTC 4618
Qy 106 ArgArgGluAenGluGlyTyrPheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 4617 AGCAAGGAAACGAGGCTACTATTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTC 4558
Qy 126 SerHisPheValProValPheLeuProAlaLysProThrThr---ProAlaProArg 144
Db 4557 AGTTCTGTCGTGCGCAGCTCTTTCAGAAAGTGAACCTACTACTACCAAGCCAGTGTGCGA 4498
Qy 145 ProProThrProAla---ProThrIleAlaSerGlnProLeuSerLeuArgProGluAla 163
Db 4497 ACTCCCTCACCTGTGCACCTACCGGACATCTCAGCCC-----CAGAGACCAGAAGAT 4444
Qy 164 CysArgPro-----AlaAlaGlyGlyAlaGlyAsnArg 174
Db 4443 TGTGCGCCCGTGGCTCAGTGAAGGGACCGGAACCGG 4405

RESULT 12
US-08-403-853-9
; Sequence 9, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORRT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,853
; FILING DATE: 30-MAY-1995
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Alignment Scores:
Pred. No.:      1.08e-05      Length:      1479
Score:          175.50      Matches:      58
Percent Similarity: 42.3%      Conservative: 24
Best Local Similarity: 29.9%      Mismatches:  77
Query Match:      16.8%      Indels:      36
DB:              4          Gaps:         8

US-10-804-763-3 (1-198) x US-09-596-774-5 (1-1479)

Qy      1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db      449 CTGGCGGTGGCGGTCTGTGGTGGCGGTGGCTCCGGCGTGGCGGTCTGCATCCAGCTGA 508
Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db      509 CCCAGTCTCACAATTCCTGTCCACTTCA-----GTAGGAGACAGGGTCAGC 555
Qy      41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db      556 ATCACCCTGCAGGCC---AGTCAGGATGTGTATATGCTGTGCTGGTATCAACAGAAA 612
Qy      61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      613 CCAGGA-----CAATCTCTAAACTTCGTATTTACTCGGCATCTCCCGGTACACTGGA 666
Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      667 GTC-----CCTTCTCGTCTCACTGGCAGTGGCTCTGGGCGCGGATTTCACTTTC 714

```


QY 181 oArgProValValLysSerGlyAspLysPro 191
Db 1195 CTGCCAGCCCATGCTGGAGGCCACCACCA 1225

Search completed: May 29, 2006, 12:46:48
Job time : 220.633 secs

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,359
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
US-08-907-146-21

Alignment Scores:
Pred. No.: 0.133 Length: 5526
Score: 136.00 Matches: 57
Percent Similarity: 38.1% Conservative: 31
Best Local Similarity: 24.7% Mismatches: 74
Query Match: 13.0% Indels: 69
DB: 3 Gaps: 11

US-10-804-763-3 (1-198) x US-08-907-146-21 (1-5526)

QY 7 AlaLeuLeuProLeuAla-----LeuLeuLeuHisAlaAla----- 19
Db 604 GCCGTTTCTCCCTCTCTCCCTCTCCCTCTCCAGGTTCCTGGTGGCAGCGCTGACT 663
QY 20 ArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrVal 39
Db 664 CAGCGTCTCGGTGTCAACAACCG-----GGAGAAACCGTC 702
QY 40 GluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGln 59
Db 703 AAGATCACCTGC-----TCCGGGATAGGAGCTACTATGGCTGG---TACCAG 747
QY 60 ProArgGlyAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLys 79
Db 748 CAGAAAGCCAGCTGGCAGTGCCTCTCTCTATGTATGTATGTAACCAACAGACCCCTCG 807
QY 80 AlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheVal 99
Db 808 GACATC-----CCTTCAGATTCTCCGGTTCGAATCCGGCTCCACGCCACA 855
QY 100 LeuThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSer 119
Db 856 TTAAACCATCACTGGGGTCCAAGCCGACGACGAGGCTGTCTATTACTGTGGGAGTGCAGAC 915
QY 120 AsnSer-Ile----- 122
Db 916 AGCAGCAGTACTGTGTCAGGTGACACAAAGCAATGGGGAATGATACAAAACCTCCTG 975
QY 123 -----MetTyrPheSerHisPheVal-----ProValPh 132
Db 976 CCAGTGCAGAGGAGCAGTGTGTTTACTGTCTCTCTCTTACAAGTCCACCTCCATT 1035
QY 132 eLeuPro-----AlaLysProThrThrProAlaProArg----- 144
Db 1036 CTTGCCCTGTGTGTGAGCGCCCGGGTCTCTCGCGTTCACAGGCTGCACCCAGGTCCAG 1095
QY 145 -----ProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgPr 161
Db 1096 CTGGCTGAATCCCTGCCATCCAACATCCACCATTTGTAGTGTCCC----- 1141
QY 161 oGluAlaCysArgProAlaAlaGlyAlaGlyAlaGlyAsnArgArgValCysLysCysPr 181
Db 1142 -----TGCATGACACCGGTGCGAGCTCTCTCATCTCTGCTCTCCACTGAGACCAC 1194


```
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x US-10-804-762-4 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
Db 120 ATGGCCCTTACAGTGACCGCCTTGTCTCGCGTGGCTTGTCTCCAGCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGGAACCTGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGTCTCCAAACCGGACCTGCTCGTGGCTCTTCCAGCGG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGGCTGGACACCGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCCAGCGAAGCCCAACGAGG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCCACCAACCGCGCGCCACCATCGCGTGCAGACCCCTGTCTCGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGGGGTGCCGCGCAGCGCGGGGGCGGCGAGGACCGGAGACGTGTTGCAATGT 659
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 660 CCCCAGCGCTGTGGTCAATCGGGAGACAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 2
US-10-804-763-4
; Sequence 4, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-4

Alignment Scores:
Pred. No.: 6,78e-99 Length: 2150
Score: 1043.00 Matches: 198
Percent Similarity: 100.0% Conservative: 0

US-10-804-763-3 (1-198) x US-10-804-762-4 (1-2150)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHieAlaAlaArg 20
Db 120 ATGGCCCTTACAGTGACCGCCTTGTCTCGCGTGGCTTGTCTCCAGCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGGACCTGGGAACCTGGGCGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTCCAGGTGCTGTCTCCAAACCGGACCTGCTCGTGGCTCTTCCAGCGG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGCGCGCGCGCGCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGGCTGGACACCGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTCGTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGGACTTCCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCTGCCAGCGAAGCCCAACGAGG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGCGGACCCACCAACCGCGCGCCACCATCGCGTGCAGACCCCTGTCTCGCGC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyAlaGlyAsnArgArgValCysLysCys 180
Db 600 CCAGAGGGGTGCCGCGCAGCGCGGGGGCGGCGAGGACCGGAGACGTGTTGCAATGT 659
Qy 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 660 CCCCAGCGCTGTGGTCAATCGGGAGACAAGCCAGCCCTTTCGCGGAGATACGTC 713

RESULT 3
US-10-804-762-28
; Sequence 28, Application US/10804762
; Publication No. US20050042217A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Specific Inhibition of Allotransplantation
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00005)
; CURRENT APPLICATION NUMBER: US/10/804,762
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-762-28

Alignment Scores:
Pred. No.: 1.17e-95 Length: 708
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
```



```
Query Match: 96.5% Indels: 37
DB: 9 Gaps: 1

US-10-804-763-3 (1-198) x US-10-804-762-28 (1-708)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 1 ATGGGCTTACCAAGTACCGCCCTTGCTCCGCGCTGGCTTGTGCTCCACGCCGCGCAG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 61 CCGAGCCAGTTCCGGGTGTGCGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 120
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 121 CTGAAGTGCAGGTGCTGCTCCAAACCGACGCTGGGCTGCTGGTGGCTCTTCCAGCG 180
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 181 CGCGGCGCGCGCGCGGCTCCACCTTCTCTCTATACCTCTCCAAAACAGCCCAAGCG 240
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 241 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTCCTC 300
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
DB 301 ACCCTGAGCGACTTCCGCGCGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 360
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 361 TCCATCATGTACTTCAGCCACATCCGCGCGGCTCTCTGCCAGCGAAGCCACACGAGCG 420
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 421 CCAGCGCGCGGACCAACACCGCGCGCCACCATCGCGTCCGACGCCCTGTCCTCGCGC 480
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 481 CCAGAGGCGTGCGCGCCAGCGCGGGGGCGGCGAGTGCACACAGGGGGGCTGGACTTCGCC 540
QY 171 ----- 171
DB 541 TGTGATATCTACATCTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTCTGTCACTG 600
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 601 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTTGTGCAATGTCCCGGCGCT 660
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
DB 661 GTGGTCAATCGGAGACAAAGCCAGCCCTTTTCGGCGAGATACGTC 705

RESULT 5
US-10-207-655-173
; Sequence 173, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
```

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; SEQ ID NO 173
; LENGTH: 1060
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-173

Alignment Scores:
Pred. No.: 1.94e-95 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 6 Gaps: 1

US-10-804-763-3 (1-198) x US-10-207-655-173 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACCAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCGAG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTCGGCTGATCGGCTGGACCTGGGAGAGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGCTGCTGCTCCAGCGC 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACCAAGCCAGCG 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCGTCCTC 365

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAAC 425

Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 426 TCCATCATGTACTTACGACCTTCTGCGGGTCTTCTGCCAGCAAGCCACACGACG 485

Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 486 CCAGCGCGCGACCAACCAACCGCGGCCACCATCGGTCGCGAGCCCTGTCTCCCTGCGC 545

Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 546 CCAGAGCGGTGCGCGCCAGCGCGCGGGCGCGCAGTGCACAGAGGGGGCTGGACTTCGCC 605

Qy 171 ----- 171
Db 606 TGTGATATCTACATCTGGGGCGCCCTTGGCCGGGACTTGTGGGGTCTTCTCTGTCACTG 665

Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 666 GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGTTGTCAAAATGTCCCGGCT 725

Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 726 GTGGTCAATCGGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 770

RESULT 6
US-10-641-643-1014
; Sequence 1014, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1014:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179145
; SEQUENCE DESCRIPTION: SEQ ID NO: 1014 :
US-10-641-643-1014

Alignment Scores:
Pred. No.: 1.94e-95 Length: 1060
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 8 Gaps: 1

US-10-804-763-3 (1-198) x US-10-641-643-1014 (1-1060)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 66 ATGGCTTACCAGTACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCGAG 125

Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 126 CCGAGCCAGTTCCGGGTGTCGGCTGATCGGCTGGACCTGGGAGAGACAGTGGAG 185

Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 186 CTGAAGTCCAGGTGCTGCTGCCAACCCGACGTCGGCTGCTGCTCCAGCGC 245

Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 246 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCAAAACCAAGCCAGCG 305

Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 306 GCCAGGGGGCTGGACACCCAGCGGTCTCGGCAAGAGGTTGGGGGACACCTTCGTCCTC 365

Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 366 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCGCTGAGCAAC 425
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QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
DB 426 TCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGCGAAGCCACACGAGC 485
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 486 CCAGCGCCGCGACCAACACACGCGGCCCCACCATCGCGTCGCGAGCCCTGTCCCTGCGC 545
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 546 CCAGAGCGGTGCGGCCACGCGCGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCC 605
QY 171 ----- 171
DB 605 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCTC 665
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 666 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCCCGGCT 725
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
DB 726 GTGGTCAATCGGGAGACAGCCAGCCCTTTCCGGGAGATACGTC 770

```

RESULT 7

US-10-804-762-2

; Sequence 2, Application US/10804762

; Publication No. US20050042217A1

; GENERAL INFORMATION:

; APPLICANT: QI, Yan

; APPLICANT: Zhang, Xianghua

; APPLICANT: Konigsberg, Paula

; TITLE OF INVENTION: Specific Inhibition of Allotransplantation

; FILE REFERENCE: A-72186/TAL/DCF (471702-00005)

; CURRENT APPLICATION NUMBER: US/10/804,762

; PRIOR FILING DATE: 2004-03-19

; PRIOR APPLICATION NUMBER: US 60/456,378

; PRIOR FILING DATE: 2003-03-19

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 2261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-804-762-2

Alignment Scores:

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Pred. No.: 4,94e-95 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 9 Gaps: 1

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US-10-804-763-3 (1-198) x US-10-804-762-2 (1-2261)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 120 ATGGCTTTACCAAGTACCGCCCTTGTCTCGCGCTGGCGCTTGTCTCCACGCCCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 180 CCGAGCCAGTTCGCGGTGCGCGCTGGATCGACCTGGAACTGGCGGAGACAGTGGAG 239
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 240 CTGAAGTGCAGGTCTGCTGTCTCAACCCGACGCTGGGCTGCTGTGGCTCTTCCAGCGC 299
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 300 CGCGCGCGCGCGCGAGTCCACCTTCTCTCTATACCTCTCTCCAAAAAAGCCCAAGGCG 359

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QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 360 GCGGAGGGGCTGACACACCGAGCGTTCGCGGCAAGAGGTTGGGGGACACCTTCGTCTC 419
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 420 ACCCTTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTCTGCTCGGCCCTGAGCAAC 479
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
DB 480 TCATCATGTACTTCAGCCACTTCGTGCGCGTCTTCCTGCCAGGAGCCACACGAGC 539
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 540 CCAGCGCCGCGACCAACACACGCGGCCCCACCATCGCGTCGCGAGCCCTGTCCCTGCGC 599
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 600 CCAGAGCGGTGCGGCCACGCGCGGGGGCGGAGTGCACACGAGGGGGTGGACTTCGCC 659
QY 171 ----- 171
DB 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCTC 719
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
DB 720 GTTATCACCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAATGTCCCGGCT 779
QY 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
DB 780 GTGGTCAATCGGGAGACAGCCAGCCCTTTCCGGGAGATACGTC 824

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RESULT 8

US-10-888-313A-99

; Sequence 99, Application US/10888313A

; Publication No. US20050100934A1

; GENERAL INFORMATION:

; APPLICANT: AXEL, Richard

; APPLICANT: LEE, Kevin

; APPLICANT: STRAPPS, Walter

; APPLICANT: BARNEA, Gilad

; TITLE OF INVENTION: Method For Assaying Protein-Protein Interaction

; FILE REFERENCE: SENTI 203.2

; CURRENT APPLICATION NUMBER: US/10/888,313A

; CURRENT FILING DATE: 2004-07-09

; PRIOR APPLICATION NUMBER: 60/566,113

; PRIOR FILING DATE: 2004-04-27

; PRIOR APPLICATION NUMBER: 60/511,918

; PRIOR FILING DATE: 2003-10-15

; PRIOR APPLICATION NUMBER: 60/485,968

; PRIOR FILING DATE: 2003-07-09

; NUMBER OF SEQ ID NOS: 101

; SEQ ID NO 99

; LENGTH: 2261

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-888-313A-99

Alignment Scores:

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Pred. No.: 4,94e-95 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 10 Gaps: 1

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US-10-804-763-3 (1-198) x US-10-888-313A-99 (1-2261)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 120 ATGGCTTTACCAAGTACCGCCCTTGTCTCGCGCTGGCGCTTGTCTCCACGCCCGCAGG 179
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40

```

Db 180 CCGAGCCAGTTCCTGGGCTGCGCGCTGGATCGGACCTGGAAACCTGGGGGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTGTCTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGTCGCGGTCTTCTGCGCAGGAGCCACCCAGCAAC 479
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCGCAGGAGCCACCCAGCAG 539
Qy 141 ProGluAlaCysArgProAlaAlaGlyGlyAla 171
Db 600 CCAGAGGGCTGCCGCGCACGCGGGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCC 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATCACCTTTACTGCAACACAGGAACCGAAGACGTGTTGCAAAATGCCCCGGCCT 779
Qy 184 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAATCGGAGACAGCCAGCCTTTCGGCGAGATAGCTC 824

RESULT 9

US-10-804-763-2
; Sequence 2, Application US/10804763
; Publication No. US20050118676A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Yan
; APPLICANT: Zhang, Xianghua
; APPLICANT: Konigsberg, Paula
; TITLE OF INVENTION: Gene Therapy Vectors Having Reduced Immunogenicity
; FILE REFERENCE: A-72186-1/TAL/DCF (471702-00008)
; CURRENT APPLICATION NUMBER: US/10/804,763
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/456,378
; PRIOR FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-804-763-2

Alignment Scores:
Pred. No.: 4,94e-95 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 10 Gaps: 1

US-10-804-763-3 (1-198) x US-10-804-763-2 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHlaAlaArg 20
Db 120 ATGGCCCTTACAGTGAGCGGCTTGTCTGCGCTGGCTTGTCTGCTCCAGCCCGCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 180 CCGAGCCAGTTCCTGGGCTGCGCCCTGGATCGGACCTGGAAACCTGGGGGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGCGCGCGCGCAGTCCACCTTCTCTATACCTTCTCCCAAAACAAGCCCAAGGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTTGGGGGACACCTTGTCTCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTTCGTCGCGGAGACAGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 479
Qy 121 SerLeuMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTGCGCAGGAGCCACCCAGCAG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGAGGGCTGCCGCGCACGCGGGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCC 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla 171
Db 600 CCAGAGGGCTGCCGCGCACGCGGGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCC 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGGCGGCCCTTGGCGGGGACTTGTGGGGTCTTCTCTGTCACTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATCACCTTTACTGCAACACAGGAACCGAAGACGTGTTGCAAAATGCCCCGGCCT 779
Qy 184 ValVallysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAATCGGAGACAGCCAGCCTTTCGGCGAGATAGCTC 824

RESULT 10

US-10-378-393-2
; Sequence 2, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-378-393-2

Alignment Scores:

Pred. No.: 2,91e-87 Length: 692
Score: 926.50 Matches: 181
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.8% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-2 (1-692)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 36 ATGGGCTTACCAAGTACCGCTTGTCTCCGCTGGCTTGTCTCCACGCCGCGAG 95
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyLnuThrValGlu 40
DB 96 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 155
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 156 CTGAAGTGCAGGTGCTGTCTCCAAACCGACGTGGGGTGTCTGGGTCTTCCAGCGG 215
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 216 CGCGGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAACAAAGCCAGGCG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 276 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 335
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 336 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTGGCCCTTGACAC 395
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 396 TCCATCATGTACTTCAGGCACATTCGTGGCGGTCTCTCCGCCAGCAAGCCACACGAGC 455
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 456 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGACACGAGGGGTGGACTTCGCC 515
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 516 CCAGAGGGGTGCGCGCCACACCGCGGGGGCGGCGAGTGCACACGAGGGGTGGACTTCGCC 575
QY 171 ----- 171
DB 576 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 635
QY 172 -----GlyAsnArgArgArgValCysLysCysProArg 182
DB 636 GTTATCACCTTTACTGCAACACACGAGAACCGAAGACGTGTTTGCAAAATGTCGCCGG 692

RESULT 11

US-10-378-393-6

; Sequence 6, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6

; LENGTH: 1995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-6

Alignment Scores:

Pred. No.: 1.08e-86 Length: 1995
Score: 926.50 Matches: 181
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.8% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-6 (1-1995)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 53 ATGGGCTTACCAAGTACCGCTTGTCTCCGCTGGCTTGTCTCCACGCCGCGAG 112
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyLnuThrValGlu 40
DB 113 CCGAGCCAGTTCCGGGTGTCGGCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 172
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 173 CTGAAGTGCAGGTGCTGTCTCCAAACCGACGTGGGGTGTCTGGGTCTTCTCCAGCGG 232
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 233 CGCGGCGCGCGCGCAGTCCCACTTCTCTATACCTCTCCCAAAACAAAGCCAGGCG 292
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 293 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGACACCTTCGTCTCTC 352
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
DB 353 ACCCTGAGGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTGGGCCCTTGACCAAC 412
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
DB 413 TCCATCATGTACTTCAGGCACATTCGTGGCGGTCTCTCCGCCAGCAAGCCACACGAGC 472
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 473 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTGCGACACGAGGGGTGGACTTCGCCG 532
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 533 CCAGAGGGGTGCGCGCCACACCGCGGGGGCGGCGAGTGCACACGAGGGGTGGACTTCGCC 592
QY 171 ----- 171
DB 593 TGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCTGCTG 652
QY 172 -----GlyAsnArgArgArgValCysLysCysProArg 182
DB 653 GTTATCACCTTTACTGCAACACACGAGAACCGAAGACGTGTTTGCAAAATGTCGCCGG 709

RESULT 12

US-10-378-393-10

; Sequence 10, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED

; TITLE OF INVENTION: TYROSINE KINASE RECEPTORS
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 2411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-10

Alignment Scores:
Pred. No.: 1,54e-86 Length: 2411
Score: 926.00 Matches: 184
Percent Similarity: 76.2% Conservatives: 2
Best Local Similarity: 75.4% Mismatches: 6
Query Match: 88.8% Indels: 52
DB: 7 Gaps: 2

US-10-804-763-3 (1-198) x US-10-378-393-10 (1-2411)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 36 ATGGCTTACCAGTGACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGACCTGGAACTGGGGGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGTCGGGCTGCTGTGCTCTTCCAGCG 215
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCGAGGTTCTGGGCAAGAGTTGGGGGACACCTTCTGCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCTTGAGCAAC 395
Qy 121 SerLeuMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 455
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTGCTCCCTGCGC 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 516 CCAGAGGGCTGCCGCGCGCGCGGGGGGCGAGTGCACAGGGGGCTGGACTTCGCC 575
Qy 171 ----- 171
Db 576 TGTGATATATCATCTGGCGCGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTGCACTG 635
Qy 172 -----GlyAsnArgArgArgValCysLysCysPro----- 181
Db 636 GTTATCACCTTTACTGCAACACACAGGAACCGAGACGTGTTGCAATGTCCTCCAG 695
Qy 182 -----ArgProValLysSerGly 188
Db 696 TCTACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCCTGACACCTAGCGGA 755
Qy 189 AspLysProSer 192

Db 756 GCGATGCCCAAC 767
RESULT 13
US-10-378-393-19
; Sequence 19, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-19

Alignment Scores:
Pred. No.: 9,72e-87 Length: 689
Score: 921.50 Matches: 180
Percent Similarity: 82.6% Conservatives: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.4% Indels: 37
DB: 7 Gaps: 1

US-10-804-763-3 (1-198) x US-10-378-393-19 (1-689)

Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 36 ATGGCTTACCAGTGACCGCTTGTCTCGCGCTGGCTTGTCTCCAGCGCCAGG 95
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCCGGGTGTCCCGCTGGATCGACCTGGAACTGGGGGAGACAGTGGAG 155
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGTCGGGCTGCTGTGCTCTTCCAGCG 215
Qy 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGCGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 275
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCCGAGGGGCTGGACACCGAGGTTCTGGGCAAGAGTTGGGGGACACCTTCTGCTC 335
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGCTACTATTCTGCTCGGCTTGAGCAAC 395
Qy 121 SerLeuMetTyPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCTATACCTCTCCCAAAACAAGCCCAAGCG 455
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 456 CCAGCGCGCGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTGCTCCCTGCGC 515
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 516 CCAGAGGGCTGCCGCGCGCGCGGGGGGCGAGTGCACAGGGGGCTGGACTTCGCC 575

QY 171 ----- 171
Db 576 TGTGATATCTACATCTGGGGCCCTTGGCGGGACTTGTGGGTCTCTTCTGTGTCTG 635
QY 172 -----GlyAsnArgArgArgValCysLysCysPro 181
Db 636 GTTATCACCCCTTTACTGCAACACACAGAACCGAAGACGTGTTTGCAAAATGTCCC 689
RESULT 14
US-10-378-393-12
; Sequence 12, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-12
Alignment Scores:
Pred. No.: 9,738-87 Length: 690
Score: 921.50 Matches: 180
Percent Similarity: 82.6% Conservative: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.4% Indels: 37
DB: 7 Gaps: 1
US-10-804-763-3 (1-198) x US-10-378-393-12 (1-690)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 36 ATGGCCTTACCAGTAGCCGCTTGCTCTGCGCGCTGGCCTTGCTGCTCCACGCCGCCAGG 95
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 155
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 156 CTGAAGTGCAGGTGCTGTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCCG 215
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 216 CGCGGCGCGCGCCAGTCACCTCTCTATATACCTCTCCAAAAAAGAGCCCAAGGGG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 276 GCGGAGGGGCTGGACACCGGGTTCGGGCAAGAGGTTGGGGGACACCTTCGTCTCTC 335
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 336 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGGTACTATTTCTGCTCGGCCCTTGAGCAAC 395
QY 121 SerIleMetTyrPheSerHisPheValProValPheProAlaLysProThrThrThr 140
Db 396 TCCATCATGACTTCAGGCACCTTCGTGGCGGTCTTCCTGCCAGCGAAGCCCAACACGAGC 455
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 456 CCAGCGCGCGACCCACCAACCGCGCCACCATCGCTCGAGCCCTGTCCCTGGCG 515
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 516 CCAGAGGCGTGC CGCGCAGCGCGGGCGGCGAGTGCACACGAGGGGGGTGGACTTCGCC 575
QY 171 ----- 171
Db 576 TGTGATATCTACATCTGGGGCCCTTGGCGGGACTTGTGGGTCTCTTCTGTGTCTG 635
QY 172 -----GlyAsnArgArgArgValCysLysCysPro 181
Db 636 GTTATCACCCCTTTACTGCAACACACAGAACCGAAGACGTGTTTGCAAAATGTCCC 689
RESULT 15
US-10-378-393-17
; Sequence 17, Application US/10378393
; Publication No. US20030182668A1
; GENERAL INFORMATION:
; APPLICANT: Bol, David K.
; APPLICANT: Carboni, Joan M.
; APPLICANT: Rowley, Ronald B.
; APPLICANT: Wong, Tai W.
; APPLICANT: Lee, Francis Y.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMALS EXPRESSING CONSTITUTIVELY ACTIVATED
; FILE REFERENCE: D0254 NP
; CURRENT APPLICATION NUMBER: US/10/378,393
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,889
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-378-393-17
Alignment Scores:
Pred. No.: 3,618-86 Length: 1987
Score: 921.50 Matches: 180
Percent Similarity: 82.6% Conservative: 0
Best Local Similarity: 82.6% Mismatches: 1
Query Match: 88.4% Indels: 37
DB: 7 Gaps: 1
US-10-804-763-3 (1-198) x US-10-378-393-17 (1-1987)
QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 37 ATGGCCTTACCAGTAGCCGCTTGCTCTGCGCGCTGGCCTTGCTGCTCCACGCCGCCAGG 96
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 97 CCGAGCCAGTTCGGGGTGTGGCGCTGGATCGGACCTGGAACTGGGCGAGACAGTGGAG 156
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 157 CTGAAGTGCAGGTGCTGTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCCG 216
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 217 CGCGGCGCGCGCCAGTCACCTCTCTATATACCTCTCCAAAAAAGAGCCCAAGGGG 276
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 277 GCGGAGGGGCTGGACACCGCGGTTCCTGCGGCAAGAGGTTGGGGGACACCTTCGTCTC 336
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db 337 ACCCTGAGCGACTTCCGCGGAGAGAACGAGGGGTACTATTTCTGCTCGGCCCTTGAGCAAC 396

GenCore version 5.1.8
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:15:35 ; Search time 19.6628 Seconds
(without alignments)
1705.079 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 242596 seqs, 56442199 residues

Total number of hits satisfying chosen parameters: 485192

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/abss/ABSSWEB.spool/US10804763/runat_26052006.165105.14645/app_query.fasta_1
-DB=Published Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -HOST=abs06p
-USER=US10804763 @CGN 1.1.39 @runat_26052006.165105.14645 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRAADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New.*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | ID | Description |
|------------|--------|-------------|------|-------------------|
| 1 | 1006.5 | 96.5 | 2261 | US-10-511-937-415 |
| 2 | 140.5 | 13.5 | 1912 | Sequence 415, App |
| 3 | 122 | 11.7 | 944 | Sequence 1818, Ap |
| 4 | 120 | 11.5 | 720 | Sequence 1585, Ap |
| 5 | 120 | 11.5 | 2081 | Sequence 39, Appl |
| 6 | 118 | 11.3 | 337 | Sequence 2348, Ap |
| 7 | 117 | 11.2 | 707 | Sequence 35, Appl |
| 8 | 115 | 11.0 | 720 | Sequence 19, Appl |
| 9 | 114 | 10.9 | 720 | Sequence 7, Appl |
| | | | | Sequence 15, Appl |

| | | | | | | |
|----|-------|------|------|---|--------------------|-------------------|
| 10 | 113 | 10.8 | 336 | 7 | US-11-211-917-3 | Sequence 3, Appl |
| 11 | 113 | 10.8 | 720 | 7 | US-11-211-917-55 | Sequence 55, Appl |
| 12 | 112 | 10.7 | 336 | 7 | US-11-211-917-11 | Sequence 11, Appl |
| 13 | 112 | 10.7 | 336 | 7 | US-11-211-917-93 | Sequence 93, Appl |
| 14 | 112 | 10.7 | 722 | 6 | US-10-503-433B-22 | Sequence 22, Appl |
| 15 | 112 | 10.7 | 796 | 6 | US-10-503-433B-24 | Sequence 24, Appl |
| 16 | 111.5 | 10.7 | 885 | 7 | US-11-154-103-33 | Sequence 33, Appl |
| 17 | 111 | 10.6 | 337 | 7 | US-11-211-917-51 | Sequence 51, Appl |
| 18 | 110.5 | 10.6 | 792 | 6 | US-10-503-433B-21 | Sequence 21, Appl |
| 19 | 110 | 10.5 | 337 | 7 | US-11-239-308-15 | Sequence 15, Appl |
| 20 | 110 | 10.5 | 704 | 6 | US-10-503-433B-15 | Sequence 15, Appl |
| 21 | 110 | 10.5 | 801 | 6 | US-10-503-433B-14 | Sequence 14, Appl |
| 22 | 109 | 10.5 | 764 | 6 | US-10-503-433B-11 | Sequence 11, Appl |
| 23 | 108 | 10.4 | 720 | 7 | US-11-211-917-31 | Sequence 31, Appl |
| 24 | 108 | 10.4 | 720 | 7 | US-11-211-917-63 | Sequence 63, Appl |
| 25 | 108 | 10.4 | 720 | 7 | US-11-211-917-79 | Sequence 79, Appl |
| 26 | 108 | 10.4 | 720 | 7 | US-11-211-917-101 | Sequence 101, App |
| 27 | 108 | 10.4 | 1954 | 7 | US-11-293-697-1648 | Sequence 1648, Ap |
| 28 | 107 | 10.3 | 795 | 6 | US-10-503-433B-12 | Sequence 12, Appl |
| 29 | 106 | 10.2 | 336 | 7 | US-11-211-917-27 | Sequence 27, Appl |
| 30 | 106 | 10.2 | 337 | 7 | US-11-211-917-75 | Sequence 75, Appl |
| 31 | 106 | 10.2 | 337 | 7 | US-11-211-917-55 | Sequence 55, Appl |
| 32 | 106 | 10.2 | 608 | 7 | US-11-301-554-908 | Sequence 908, App |
| 33 | 106 | 10.2 | 706 | 6 | US-10-503-433B-17 | Sequence 17, Appl |
| 34 | 106 | 10.2 | 4027 | 7 | US-11-169-140-1 | Sequence 1, Appl |
| 35 | 105.5 | 10.1 | 729 | 7 | US-11-154-103-20 | Sequence 20, Appl |
| 36 | 105 | 10.1 | 330 | 7 | US-11-254-679-59 | Sequence 59, Appl |
| 37 | 105 | 10.1 | 431 | 1 | US-09-784-950-71 | Sequence 71, Appl |
| 38 | 105 | 10.1 | 732 | 6 | US-10-503-433B-16 | Sequence 16, Appl |
| 39 | 104.5 | 10.0 | 2476 | 6 | US-10-196-749-585 | Sequence 585, App |
| 40 | 104 | 10.0 | 444 | 1 | US-09-784-950-63 | Sequence 63, Appl |
| 41 | 104 | 10.0 | 543 | 7 | US-11-301-554-970 | Sequence 970, App |
| 42 | 104 | 10.0 | 705 | 7 | US-11-211-917-23 | Sequence 23, Appl |
| 43 | 104 | 10.0 | 803 | 6 | US-10-503-433B-20 | Sequence 20, Appl |
| 44 | 103.5 | 9.9 | 5137 | 6 | US-10-505-928-802 | Sequence 802, App |
| 45 | 103 | 9.9 | 330 | 7 | US-11-254-679-43 | Sequence 43, Appl |

ALIGNMENTS

RESULT 1
US-10-511-937-415
; Sequence 415, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 415
; LENGTH: 2261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-415

Alignment Scores:

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Pred. No.: 2 37e-70 Length: 2261
Score: 1006.50 Matches: 197
Percent Similarity: 83.8% Conservative: 0
Best Local Similarity: 83.8% Mismatches: 1
Query Match: 96.5% Indels: 37
DB: 6 Gaps: 1

US-10-804-763-3 (1-198) x US-10-511-937-415 (1-2261)
Qy 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 120 ATGGCCCTTACAGTACCGCCCTTCTCTCGCTGGCTTGTCTCCAGCCGCCAGG 179
Qy 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGluThrValGlu 40
Db 180 CCGAGCCAGTTCGGGTGTCGGCTGGATCGACCTCGAACCTGGGGGAGACAGTGGAG 239
Qy 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 240 CTGAAGTGCCAGGTGCTGCTGCCAACCCGACGTCGGGCTCTCTCGTGGCTCTTCCAGCG 299
Qy 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 300 CGCGGGCGCGCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGCG 359
Qy 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 360 GCCGAGGGGCTGGACACCCAGCGGTTCTCGGCGAAGAGGTTGGGGGACACCTTCGTCCTC 419
Qy 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsn 120
Db 420 ACCCTGAGCGACTCCCGCGAGAGAACAGGGCTACTATTCTGCTCGGCCCTTGAGCAAC 479
Qy 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db 480 TCCATCATGTACTTACGACACTTCTGTCGGGTCTCTCCGACGAGAACCCACACGACG 539
Qy 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 540 CCAGCGCGGACACCAACACCGCGGCCACCATCGCGTGGCAGCCCTGTCCCTGGCG 599
Qy 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 600 CCAGAGGCGTCCGCGCCAGCGCGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCC 659
Qy 171 ----- 171
Db 660 TGTGATATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTTCTCTGTCACTG 719
Qy 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 720 GTTATCACCCCTTTACTGCAACACACAGGAACCGAGACGTGTTGCAATGTCCTCCGCGCT 779
Qy 184 ValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 780 GTGGTCAAAATCGGAGAGAACGCCAGCCAGCTTTCGGCGAGATACGTC 824
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RESULT 2

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US-11-293-697-1818
; Sequence 1818, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1818
; LENGTH: 1912
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1818
Alignment Scores:
Pred. No.: 0.0105 Length: 1912
Score: 140.50 Matches: 63
Percent Similarity: 33.1% Conservative: 23
Best Local Similarity: 24.2% Mismatches: 88
Query Match: 13.5% Indels: 87
DB: 7 Gaps: 10

US-10-804-763-3 (1-198) x US-11-293-697-1818 (1-1912)
Qy 10 LeuProLeuAlaLeuLeuHisAlaAlaArg-----ProSerGlnPheArgValSer 27
Db 64 CTCCTCTCTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123
Qy 28 ProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGlnValLeuLeu 47
Db 124 CCACCCCTCAGCGTCTGGGACCCCGCGGACAGCGGTCCACATCACCCTGTTCAGGAACACG 183
Qy 48 SerAsn---ProThrSerGlyCysSerTrpLeuPheGlnProArgGlyAlaAlaAlaSer 66
Db 184 TCCAAATCGAAGAAACGCTGTTAATTTGGTACGACCAAGTCCCGAGGGGAGGCC----- 237
Qy 67 ProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGluGlyLeuAspThr 86
Db 238 CCCAAATCTCTCATCTATGATTCTTATCGACGGCCCTCAGGGGTC-----CCT 285
Qy 87 GlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuLeuSerAspPheArg 106
Db 286 TCCGATTTCTCTGGCTCCAACTCTGGAACCTCAGCCTCTCTCTCTCTCTCTCTCTCTCT 345
Qy 107 ArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSer-----AsnSerIleMet 123
Db 346 TCTGACGATGAGGGTTTATTTCTGTCGCCATGGGACAGGGGCTGAATGGTCTTCTC 405
Qy 124 TyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAlaPro 143
Db 406 TTCGGCGGA-----GGGACCAAGCTGACCGTCTCTGAGTGAGTCC 444
Qy 144 ArgProProThrProAlaProThrIleAlaSerGlnProLeu----- 157
Db 445 TCTCCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 503
Qy 158 -----SerLeuArgProGlu 162
Db 504 TCTTTTTCAGATGTCCTCGGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 563
Qy 163 AlaCysArg----- 165
Db 564 GCCTCTCTGTTTCAGACACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 623
Qy 166 ProAlaAlaGlyGlyAlaGlyAsnArgArg----- 176
Db 624 CCGCAGGGTCCGGGACCCAGCAACAGACACCGTCTGAGGCTCTGTCTGTCTGTCTGTCT 683
Qy 177 -----ValCysLysCysProArgProValValLys----- 186
Db 684 CTCCTTTCTGTTCTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 743
Qy 187 -----SerGlyAspLysProSerLeuSerAlaAlaArg 196
Db 744 CCTCAGACTCAGAAAGCCCGCAAGAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 803

RESULT 3
US-11-293-697-1585
; Sequence 1585, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
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; LENGTH: 720

Db 499 GTACACTGGTATCAGCAGCTCCAGGAGCGCC-----CCCAAACTCTCATCTATGTT 552
QY 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 553 AACAAACATCGGCCTCAGGGTTC-----CCTGACCGATCTCTGGCTCCAAG 600
QY 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyr 113
Db 601 TCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTAT 660
QY 114 PheCysSerAlaLeuSerAsnSerIleMetTyrPhe 125
Db 661 TACTGTGGCGCTCTTGATGACACTGTAAGTGGTAC 696

RESULT 8

US-11-211-917-7
; Sequence 7, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-7

Alignment Scores:
Pred. No.: 0.308 Length: 720
Score: 115.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 11.0% Indels: 10
DB: 4
Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-7 (1-720)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTGGGGCTGCTAAGTCTCTGGATCCAGTGGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGCTGACTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGCGCGCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGCAGGTCTAGTCAGAGCCTCTGTATAGTATGATGATCAACATTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCCAGGG-----CAGTCTCCACAGCTCTCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGGTCC---CCTGACAGGTTTCAGTGGCAGTGATGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTC 339

RESULT 10

US-11-211-917-3
; Sequence 3, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40

Db 283 GATTTTACACTGAAATCAGCAGATTTGAGGCTGAGGATGTTGGGGTTTATTACTGTC 339

RESULT 9

US-11-211-917-15
; Sequence 15, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2005-08-25
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-15

Alignment Scores:
Pred. No.: 0.368 Length: 720
Score: 114.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 10.9% Indels: 10
DB: 4
Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-15 (1-720)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTGGGGCTGCTAAGTCTCTGGATCCAGTGGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCAACCCCTGGAGCGCGCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTCGCAGGTCTAGTCAGAGCCTCTGTATAGTATGATGATCAACATTTTGGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCCAGGG-----CAGTCTCCACAGCTCTCTGATCTATTGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCTCCGGGGTCC---CCTGACAGGTTTCAGTGGCAGTGATGATCAGGCACA 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTC 339

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; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-3

Alignment Scores:
Pred. No.: 0.171 Length: 336
Score: 113.00 Matches: 32
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 10.8% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-3 (1-336)

QY 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTCGGCTCAGTCCAGAGCGGCTCCATCTCTCGCAGGTCTAGT 78
QY 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCCTCTGTATAGTAATGGATACAACTTTTGGATTTGGTACCTCGCAGAGCCAGGG 138
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCTGATCTATTGGTCTTAATCGG-----GCCCTCC 183
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 103 SerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 241 AGCAGATTGGAGGCTGAGGATGTTGGGTTTATTACTGC 279

RESULT 11
US-11-211-917-55
; Sequence 55, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-11

Alignment Scores:
Pred. No.: 0.205 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 10.7% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-11 (1-336)

QY 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCCACTCTCCCTCGGCTCAGTCCAGAGCGGCTCCATCTCTCGCAGGTCTAGT 78
QY 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCCTCTGTATAGTAATGGATACAACTTTTGGATTTGGTACCTCGCAGAGCCAGGG 138
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCTGATCTATTGGTCTTAATCGG-----GCCCTCC 183
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 103 SerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 241 AGCAGATTGGAGGCTGAGGATGTTGGGTTTATTACTGC 279

RESULT 12
US-11-211-917-11
; Sequence 11, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; CURRENT FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-11

Alignment Scores:
Pred. No.: 0.205 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 10.7% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-55 (1-720)

QY 1 MetalAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTCGGGCTGCTAATGCTCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTGCAGGCTTAGTCAGAGCTCTCTGTATAGTAATGATATACTATTTCGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCCAGG-----CAGTCTCCACACCTCTCTGATCTATTTCGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC---CCTGACAGGTTTCAGTGGCAGTGGTTTCAGGCAC 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGC 339

Score: 113.00 Matches: 37
Percent Similarity: 42.9% Conservative: 14
Best Local Similarity: 31.1% Mismatches: 58
Query Match: 10.8% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-55 (1-720)

QY 1 MetalAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHiAlaAlaArg 20
Db 1 ATGAGGCTCCCTGCTCAGCTCTCGGGCTGCTAATGCTCTCTGGTCTCTGGATCCAGTGG 60
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGCCCTCC 120
QY 41 LeuLysCysGln-----ValLeuLeuSerAsnProThrSerGlyCysSerTrp 56
Db 121 ATCTCTGCAGGCTTAGTCAGAGCTCTCTGTATAGTAATGATATACTATTTCGATTGG 180
QY 57 LeuPheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyTrpLeuSerGlnAsn 76
Db 181 TACCTGCAGAACCCAGG-----CAGTCTCCACACCTCTCTGATCTATTTCGGTTCTAAT 234
QY 77 LysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAsp 96
Db 235 CGG-----GCCCTCGGGGTC---CCTGACAGGTTTCAGTGGCAGTGGTTTCAGGCAC 282
QY 97 ThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCys 115
Db 283 GATTTTACACTGAAATCAGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGC 339
```



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Db 79 CAGAGCCTCTGTTATAGTAATGATCAACTTTTGGATTGGTACCTGCAGAGCCAGG 138
Qy 63 AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 241 AGCAGAGTCGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 13
US-11-211-917-93
; Sequence 93, Application US/11211917
; Publication No. US20060093600A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/11/211,917
; PRIOR FILING DATE: 2005-08-25
; PRIOR APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 93
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-211-917-93

Alignment Scores:
Pred. No.: 0.205 Length: 336
Score: 112.00 Matches: 32
Percent Similarity: 45.2% Conservative: 10
Best Local Similarity: 34.4% Mismatches: 41
Query Match: 10.7% Indels: 10
DB: 7 Gaps: 4

US-10-804-763-3 (1-198) x US-11-211-917-93 (1-336)
Qy 27 SerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLysCysGln----- 44
Db 19 TCTCACCTCTCCCTGCCGCTACCCCTGAGAGCGCGCTCCATCTCTGCAGGCTAGT 78
Qy 45 -----ValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 79 CAGAGCCTCTCTATAGTAATGATACAACTTTTGGATTGGTACCTGCAGAGCCAGG 138
Qy 63 AlaAlaAaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 139 -----CAGTCTCCACAGCTCCTGATCTATTGGGTCTTAATCGG-----GCCTCC 183
Qy 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 184 GGGGTC---CCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Qy 103 SerAspPheArgGluAsnGluGlyTyrTyrPheCys 115
Db 241 AGCAGAGTCGAGGCTGAGGATGTTGGGGTTTATTACTGC 279

RESULT 14
US-10-503-433B-22

```

```

; Sequence 22, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 22
; LENGTH: 722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F8 mutated clone 2-20
US-10-503-433B-22

Alignment Scores:
Pred. No.: 0.53 Length: 722
Score: 112.00 Matches: 30
Percent Similarity: 48.3% Conservative: 13
Best Local Similarity: 33.7% Mismatches: 38
Query Match: 10.7% Indels: 8
DB: 6 Gaps: 3

US-10-804-763-3 (1-198) x US-10-503-433B-22 (1-722)
Qy 36 GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- 53
Db 438 GGGCAGAGGTCACCATCTCTTGCTGCGGACGAGCTCCAACTCGGGCAGGTACGAT 497
Qy 54 CysSerTrpLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu 73
Db 498 GTACACTGGTATCAGCAGCTCCAGGAAGCGCC-----CCCAAACTCTCATCTATGT 551
Qy 74 SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg 93
Db 552 AACAACTCGGCGCTCAGGGGTC-----CCTGACCGATTTCTGCTCCAAG 599
Qy 94 LeuGlyAspThrPheValLeuThrLeuSerAspPheArgGluAsnGluGlyTyrTyr 113
Db 600 TCTGCACCTCAGCCTCCCTGCGCATCAGTGGGCTCCGTCGAGATGAGGCTGATTAT 659
Qy 114 PheCysSerAlaLeuSerAsnSerIle 122
Db 660 TACTGTGCGCTTATGATGACAGTATT 686

RESULT 15
US-10-503-433B-24
; Sequence 24, Application US/10503433B
; Publication No. US20060099641A1
; GENERAL INFORMATION:
; APPLICANT: Mats OHLIN
; TITLE OF INVENTION: Method of Making Libraries of Anti-Ligands
; FILE REFERENCE: 12578/46301
; CURRENT APPLICATION NUMBER: US/10/503,433B
; PRIOR FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: PCT/EP03/00982
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: GB 0202206.9
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: SeqWin99
; SEQ ID NO 24
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

OTHER INFORMATION: F8 mutated clone 2-18
US-10-503-433B-24

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 0.598 | Length: | 796 |
| Score: | 112.00 | Matches: | 29 |
| Percent Similarity: | 49.4% | Conservative: | 15 |
| Best Local Similarity: | 32.6% | Mismatches: | 37 |
| Query Match: | 10.7% | Indels: | 8 |
| DB: | 6 | Gaps: | 3 |

US-10-804-763-3 (1-198) x US-10-503-433B-24 (1-796)

| | | | |
|----|-----|---|-----|
| Qy | 36 | GlyGluThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGly----- | 53 |
| Db | 439 | GGGAGAGGGTCACCATCTCTTGCACTGGGAGCAGCTCCAACATCGGGGAGGTTTGGAT | 498 |
| Qy | 54 | CysSerTyrLeuPheGlnProArgGlyAlaAlaSerProThrPheLeuLeuTyrLeu | 73 |
| Db | 499 | GTACACTGGTATCAGCAGCTCCAGGAACGGCC-----CCCAACTCTCATCTATGGT | 552 |
| Qy | 74 | SerGlnAsnLysProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArg | 93 |
| Db | 553 | AACAAATCGCCCTCAGGGTC-----CCTGACCGATTCTTGGCTCCAAG | 600 |
| Qy | 94 | LeuGlyAspThrPheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyr | 113 |
| Db | 601 | TCTGGCACCCTCAGCCTCCCTGGCCATCAGTGGGCTCCGGTCCGAGGATGAGGCTGATTAT | 660 |
| Qy | 114 | PheCysSerAlaLeuSerAsnSerIle | 122 |
| Db | 661 | TACTGTGGGCTCTCGATGACACTCTC | 687 |

Search completed: May 30, 2006, 04:18:02
Job time : 21.6628 secs

GenCore version 5.1.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 30, 2006, 04:13:46 ; Search time 4304.33 Seconds

(without alignments)
3858.452 Million cell updates/sec

Title: US-10-804-763-3

Perfect score: 1043

Sequence: 1 MALPVTALLPLALLHAAR.....KCPRPVVKSGDKPSLSARYV 198

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh

-O=/abs/ABSSWEB spool/US10804763/runat_26052006_165054_14448/app_query.fasta_1

-DB=EST_QPMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45

-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL

-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes04

-USER=US10804763 @CGN 1 1 7986 @runat_26052006_165054_14448 -NCPU=6 -ICPU=3

-NO WMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -FGAPOP=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hic:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 1043 | 100.0 | 1948 | 6 | CR619549 full-length |
| 2 | 1030 | 98.8 | 755 | 9 | DR007174 TC101240 |
| 3 | 1008 | 96.6 | 705 | 2 | BI905877 603063005 |
| 4 | 981.5 | 94.1 | 789 | 2 | BI19839 603041366 |

| | | | | | | |
|----|-------|------|------|---|-----------|---------------------|
| 5 | 966.5 | 92.7 | 804 | 2 | BI820808 | BI820808 603034019 |
| 6 | 963 | 92.3 | 549 | 9 | DB121562 | DB121562 DB121562 |
| 7 | 958 | 91.9 | 884 | 1 | AL552456 | AL552456 AL552456 |
| 8 | 952.5 | 91.3 | 838 | 9 | DA931234 | DA931234 DA931234 |
| 9 | 951.5 | 91.2 | 882 | 2 | BI820267 | BI820267 603036820 |
| 10 | 943.5 | 90.5 | 780 | 2 | BI760947 | BI760947 603043151 |
| 11 | 931 | 89.3 | 1109 | 4 | BX415859 | BX415859 BX415859 |
| 12 | 928 | 89.0 | 566 | 9 | DA943842 | DA943842 DA943842 |
| 13 | 900.5 | 86.3 | 949 | 8 | CO646993 | CO646993 ILLUMIGEN |
| 14 | 899 | 86.2 | 571 | 9 | DA952710 | DA952710 DA952710 |
| 15 | 899 | 86.2 | 576 | 9 | DA826683 | DA826683 DA826683 |
| 16 | 899 | 86.2 | 578 | 9 | DA956498 | DA956498 DA956498 |
| 17 | 899 | 86.2 | 576 | 9 | DA974329 | DA974329 DA974329 |
| 18 | 899 | 86.2 | 586 | 9 | DA942852 | DA942852 DA942852 |
| 19 | 899 | 86.2 | 594 | 2 | BI760884 | BI760884 603043751 |
| 20 | 899 | 86.2 | 602 | 9 | DB1110509 | DB1110509 DB1110509 |
| 21 | 899 | 86.2 | 627 | 9 | DA371487 | DA371487 DA371487 |
| 22 | 899 | 86.2 | 840 | 2 | BI835165 | BI835165 603088746 |
| 23 | 897 | 86.0 | 600 | 9 | DB117237 | DB117237 DB117237 |
| 24 | 897 | 86.0 | 606 | 9 | DA936371 | DA936371 DA936371 |
| 25 | 897 | 86.0 | 611 | 9 | DB123733 | DB123733 DB123733 |
| 26 | 895.5 | 85.9 | 796 | 2 | BI911195 | BI911195 603062918 |
| 27 | 895 | 85.8 | 589 | 9 | DA941044 | DA941044 DA941044 |
| 28 | 895 | 85.8 | 620 | 9 | DA381496 | DA381496 DA381496 |
| 29 | 893 | 85.6 | 545 | 9 | DB102835 | DB102835 DB102835 |
| 30 | 893 | 85.6 | 571 | 9 | DB106910 | DB106910 DB106910 |
| 31 | 893 | 85.6 | 577 | 9 | DB200083 | DB200083 DB200083 |
| 32 | 893 | 85.6 | 599 | 9 | DA935416 | DA935416 DA935416 |
| 33 | 893 | 85.6 | 599 | 9 | DA938336 | DA938336 DA938336 |
| 34 | 892 | 85.5 | 704 | 9 | DN997301 | DN997301 TC111602 |
| 35 | 887 | 85.0 | 596 | 9 | DA940758 | DA940758 DA940758 |
| 36 | 887 | 85.0 | 597 | 9 | DA940156 | DA940156 DA940156 |
| 37 | 887 | 85.0 | 628 | 9 | DB123661 | DB123661 DB123661 |
| 38 | 882 | 84.6 | 580 | 9 | DA946587 | DA946587 DA946587 |
| 39 | 881 | 84.5 | 585 | 9 | DB110036 | DB110036 DB110036 |
| 40 | 881 | 84.5 | 592 | 9 | DA670538 | DA670538 DA670538 |
| 41 | 881 | 84.5 | 593 | 9 | DA421985 | DA421985 DA421985 |
| 42 | 881 | 84.5 | 593 | 9 | DB110805 | DB110805 DB110805 |
| 43 | 877 | 84.1 | 567 | 9 | DB118175 | DB118175 DB118175 |
| 44 | 874 | 83.8 | 569 | 9 | DB124972 | DB124972 DB124972 |
| 45 | 873 | 83.7 | 576 | 9 | DB121098 | DB121098 DB121098 |

ALIGNMENTS

| | | | | | |
|------------|--|---------|------|--------|-----------------|
| RESULT 1 | CR619549 | 1948 bp | mRNA | linear | HTC 21-JUL-2004 |
| LOCUS | full-length cDNA clone CS0DI070YG17 of Placenta Cot 25-normalized | | | | |
| DEFINITION | of Homo sapiens (human). | | | | |
| ACCESSION | CR619549 | | | | |
| VERSION | CR619549.1 GI:50500356 | | | | |
| KEYWORDS | HTC; CNSLT_cDNA. | | | | |
| SOURCE | Homo sapiens (human) | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. | | | | |
| AUTHORS | 1 (bases 1 to 1948) | | | | |
| TITLE | Li,W.B., Gruber,C., Jesse,J. and Polayes,D. | | | | |
| JOURNAL | Full-length cDNA libraries and normalization | | | | |
| REMARK | Unpublished | | | | |
| REFERENCE | Contact : Peng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue | | | | |
| AUTHORS | 2 (bases 1 to 1948) | | | | |
| TITLE | Genoscope. | | | | |
| JOURNAL | Direct Submission | | | | |
| COMMENT | Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr) - Web : www.genoscope.cns.fr | | | | |
| | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned | | | | |

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Source

```

1. 1948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS01070YG17"
/tissue_type="placenta C
/plasmid="pCMVSPORT6"

```

ORIGIN

| | | |
|------------------------|----------|---------------|
| Alignment Scores: | | |
| Pred. No.: | 2,33e-78 | 1948 |
| Score: | 1043.00 | Matches: |
| Percent Similarity: | 100.0% | Conservative: |
| Best Local Similarity: | 100.0% | Mismatches: |
| Query Match: | 100.0% | Indels: |
| DB: | 6 | Gaps: |

US-10-804-763-3 (1-198) x CR619549 (1-1948)

| | | | |
|----|-----|--|-----|
| Qy | 1 | MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg | 20 |
| Db | 71 | ATGGCCCTTACCAAGTACCGCCCTTGCTCCGTGCGCTGGCTTGTGCTGCACGCGCGCAG | 130 |
| Qy | 21 | ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu | 40 |
| Db | 131 | CCGAGCCAGTTCGGGGTTCGCGCGTGGATCGAACCTCGGCGCAGACAGTGGAG | 190 |
| Qy | 41 | LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro | 60 |
| Db | 191 | CTGAAATGCCAGTCTGCTCTCCAAACCCGACGTCGGGTGCTGTGGCTCTTCACGCCG | 250 |
| Qy | 61 | ArgGlyValAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla | 80 |
| Db | 251 | CGCGGCGCGCGCCAGTCCCACCTTCCTCTATACCTTCCCCAAAAACAAGCCCAAGGCG | 310 |
| Qy | 81 | AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu | 100 |
| Db | 311 | GCGAGGGGCTCGACACCCAGCGGTTCTCGGGCAAGAGTTGGGGGACACCTTCGTGCTCTC | 370 |
| Qy | 101 | ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn | 120 |
| Db | 371 | ACCTTGAGCGCATTCGGCCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGACCAAC | 430 |
| Qy | 121 | SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr | 140 |
| Db | 431 | TCCATCATGTACTTCAGCCACCTTCGTGCGCGTCTTCCTGCCAGCAAGCCACACGACG | 490 |
| Qy | 141 | ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg | 160 |
| Db | 491 | CCAGCGCCGCGACCAACACCGGGCGCCACCATCGCGTCGCGAGCCCCCTGTCCCTGCGC | 550 |
| Qy | 161 | ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysCys | 180 |
| Db | 551 | CCNAGGCGGTGCGGCCACGCGCGGGGGCGCAGGGAACCGAAGACGTGTTCGCAATGT | 610 |
| Qy | 181 | ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal | 198 |
| Db | 611 | CCCGCGCTGTGTCAATTCGGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC | 664 |

| | | | | | |
|------------|--|--------|------|--------|-----------------|
| RESULT 2 | DR007174 | 755 bp | mRNA | linear | EST 17-MAY-2005 |
| LOCUS | DR007174 | | | | |
| DEFINITION | TC101240 Human spleen, large insert, pCMV expression library Homo sapiens cDNA clone TC101240 5' similar to Homo sapiens CD8 antigen, alpha polypeptide (p32) (CD8A), transcript variant 2, mRNA sequence. | | | | |
| ACCESSION | DR007174 | | | | |
| VERSION | DR007174.1 | | | | GI:66267047 |
| KEYWORDS | EST. | | | | |

```
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 277 GCGGAGGGCTGGACACCCAGCGGTTCTCGGCGAAGAGGTGGGGACACCTTCGTCTC 336
QY 101 ThrLeuSerAspPheArgGluAanGluGlyTyrPheCysSerAlaLeuSerAan 120
Db 337 ACCCTGAGGACACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTTGACAAC 396
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 397 TCCATCATGTACTTCAGGCACCTTCGTGCGCGTCTTCCTGCCAGGAAGCCACACGAGC 456
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 457 CCAGGCGCGGACCAACACCGGCGCCACCATCGCTCGCAGCCCTGTCTCTCGCGC 516
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla-GlyAanArgArgValCysLysCY 180
Db 517 CCAGAGGCGTGGCGGACGCGGGGGCGCTAGGGAACCGAAGACGTTTTCGAAATG 576
QY 180 sProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 577 TCCCGGCGCTGTGGTCAATCGGAGACAAGCCAGCCCTTCGGCGAGATACGTC 631
```

RESULT 3

```
BI905877 705 bp mRNA linear EST 16-OCT-2001
LOCUS 603063005F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212128 5',
DEFINITION mRNA sequence.
```

```
ACCESSION BI905877
VERSION BI905877.1 GI:16168472
```

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 705)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11532 row: j column: 01

High quality sequence stop: 705.

FEATURES

source

1..705

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5212128"

/tissue_type="leukocyte"

/lab_host="DH10B"

/clone_lib="NIH MGC_118"

/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV

(destroyed); RNA source leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

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Pred. No.: 6,08e-76 Length: 705
Score: 1008.00 Matches: 196
Percent Similarity: 99.0% Conservative: 0
Best Local Similarity: 99.0% Mismatches: 2
Query Match: 96.6% Indels: 1
DB: 2 Gaps: 0
```

US-10-804-763-3 (1-198) x BI905877 (1-705)

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QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 65 ATGGCCCTTACCAAGTACCGCCCTTCCTCGCGCTGGCCTTGTCTGTCCACGCCGCGCAGG 124
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAanLeuGlyGluThrValGlu 40
Db 125 CCGAGCCAGTTCGGGGTGTGCGCGCTGGATCGGACCTGGGAACCTGGCGGAGACAGTGGAG 184
QY 41 LeuLysCysGlnValLeuLeuSerAanProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 185 CTGAAGTGCAGGTGCTGTCTCAACCGAGCTCGGGCTGTCTCGTGGCTCTTCCAGCCG 244
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAanLysProLysAla 80
Db 245 CCGGGCGCGCGCGAGTCCCACCTTCCTCTATACCTCTCCCAAAACCAAGCCCAAGGCG 304
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 305 GCGGAGGGCTGGACACCCAGCGGTTCTCGGCGAAGAGGTTGGGGACACCTTCGTCTCTC 364
QY 101 ThrLeuSerAspPheArgGluAanGluGlyTyrTyrPheCysSerAlaLeuSerAan 120
Db 365 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGC-CTGAGCAAC 423
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 424 TCCATCATGTACTTCAGCCACTTCGTGCGCGGCTTCCTCGCCAGGAAGCCACACGAGC 483
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 484 CCAGCGCGCGGAGAACCAACACCGCGGCCACCATCGGTCCGACCCCTGTCTCTCTCGC 543
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAanArgArgValCysLysCys 180
Db 544 CCAGAGGCGTTCGCGGCCAGCGCGGGGGCGGAGGAAACCGAAGACGCTGTTTGCAATGT 603
QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db 604 CCCCAGCCTTGTGTCAAAATCGGGAGACAAGCCAGCCCTTTCGGCGAGATACGTC 657
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RESULT 4

BI919839

LOCUS

603041366F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182049 5',
mRNA sequence.

ACCESSION

BI919839

VERSION

BI919839.1 GI:15931389

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

1 (bases 1 to 789)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Prepared: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11532 row: j column: 01

High quality sequence stop: 705.

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM11454 row: d column: 18
High quality sequence stop: 788.

FEATURES

source

1. 789
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5182049"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 1.3e-73 Length: 789
Score: 981.50 Matches: 196
Percent Similarity: 83.1% Conservative: 0
Best Local Similarity: 83.1% Mismatches: 2
Query Match: 94.1% Indels: 38
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI819839 (1-789)

QY 1 MetaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
DB 76 ATGGCTTTACAGTACCGCTTGTCTCGCGTGGCTGTCTCTCCAGCCGACG 135
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 136 CCGAGCCAGTTCCGGGTGTCGCGTGTGATCGGACCTGGACCTGGCGGAGACGTGGAG 195
QY 41 LeuLeuGlyGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 136 CTGAAGTCCAGGTCTGTGTCACACCGACGTGGGCTGTCTCTCCAGCGG 255
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTrpLeuSerGlnAsnLeuProLysAla 80
DB 256 CGCGGCGCGCGCGCGAGTCCACCTTCTCTATACCTCTCCAAACACAGCCGAGGCG 315
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 316 CGCGAGGGGCTGACACACCGCGTTCTCGGGCAAGAGTTGGGGGACACCTTCGTCCTC 375
QY 101 ThrLeuSerAppPheArgGluAsnGluGlyTyrrPheCysSerAlaLeuSerAsn 120
DB 376 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTTCTGCTCGCGCCCTGAGCAAC 435
QY 121 SerIleMetTyrrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
DB 436 TCCATCATGTACTTCAGCACCTTCGTGCGGTCTTCTGCGAGCGAGGCCACACGAGG 495
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
DB 496 CCAGCGCGCGGACCAACACCGCGGCCACCATCGGTCGCGCCCTGTCTCTCTGCGC 555
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
DB 556 CCAGAGGGGCTGCGCGGACGCGGGGCGCAGTGCACAGAGGGGGCTGGACTTCGCG 615
QY 171 ----- 171
DB 616 CTGTGATATCTACATCTGGGCGCCCTTGGCGGGACTTGGGGGTCTCTCTCTCTCACT 675

QY 172 -----GlyAsnArgArgValCysLysCysProArgPr 183
DB 676 GGTATTACCCCTTTACTGCAACACGAGACCGAGAGCTGTTCGCAATGTCCCGGCC 735
QY 183 ovalValValSerGlyAspLysProSerLeuSerAlaArgTrpVal 198
DB 736 TGTGTCAAATCGGAGACAGCCAGCCTTTCCGCGGAGATACGTC 781

RESULT 5

BI820808 804 bp mRNA linear EST 04-OCT-2001
LOCUS 603034019F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175149 5',
DEFINITION mRNA sequence.

ACCESSION BI820808

VERSION BI820808.1 GI:15932358

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 804)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11436 Row: e column: 06

High quality sequence stop: 802.

FEATURES

Location/Qualifiers

source

1. 804

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5175149"

/lab_host="DH10B"

/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 2.55e-72 Length: 804
Score: 966.50 Matches: 190
Percent Similarity: 81.5% Conservative: 0
Best Local Similarity: 81.5% Mismatches: 6
Query Match: 92.7% Indels: 37
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI820808 (1-804)

QY 3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArgProSer 22

DB 7 TTACAGTGACCGCTTCTCTCGCTGGCTTGGCTTCCAGCGCGAGCGGAGC 66

QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42

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Db      67  CAGTTCGGGGTGTGCGCGCTGGATCGGACCTGGGAACCTGGGCGGAGACAGCTGGAGCTGAAG 126
Qy      43  CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTripleuPheGlnProArgGly 62
Db      127  TGGCAGGTGCTGCTGCCAACCGGACGTGGGGTGTCTGGTGGCTCTCCAGCGCGCGCGC 186
Qy      63  AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db      187  GCGCGCGCGCGCTCCACCTTCCTCTATACCTCTCCCAAAACAAGCCCAAGGCGCGCGAG 246
Qy      83  GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db      247  GGCTGACACCCAGCGGTTCTCGGCAAGAGGTGGGGACACCTTCGTCTCCACCTG 306
Qy      103  SerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsnSerIle 122
Db      307  AGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCACTCCATC 366
Qy      123  MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrProAla 142
Db      367  ATGTACTTCAGCCACTTCGTGCGGGTCTTCCTGCCAGCGAAGCCCAACGACGCGCAG 426
Qy      143  ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db      427  CGCGGACCAACACACCGCGGCCACCATCGGTGCGAGCCCTGTCTCTGCGCCAGAG 486
Qy      163  AlaCysArgProAlaAlaGlyGlyAla----- 171
Db      487  GCGTGCAGCGCCAGCGCGGGGGCGCAGTGACACAGAGGGGGTGGACTTCGCGCTGTGAT 546
Qy      171  ----- 171
Db      547  ATCTACATCTGGCGGCCCTTGGCGGGACTTGTGGGGTCTCTCTCTGTCTCACTGGTTATC 606
Qy      172  -----GlyAsnArgArgArgValCysLysCysProArgProValVal 185
Db      607  ACCCTTTACTGCAACACACAGGAACCGAAGACGTGTTGCAAAAGTCCCCGGCGCTGGGTC 666
Qy      186  LysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
Db      667  AAATCGGGAGACAGCCAGCCTTTCGGCGAGATAGTC 705

RESULT 6
DB121562
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 549)
Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaquri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,K., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Promoters of Human Genes
Genome Res. 16 (1), 55-65 (2006)
16344560
Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kametari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986

TITLE
JOURNAL
PUBMED
COMMENT

```

```

Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction;
Helix Research Institute (HRI); 5'-end one pass sequencing; HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
FEATURES
    source
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            Location/Qualifiers
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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="THYMU2030213"
                /tissue_type="thymus"
                /clone_lib="THYMU2"
                /note="Vector: pME18SFL3"
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Alignment Scores:
Pred. No.: 3.09e-72 Length: 549
Score: 963.00 Matches: 181
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 92.3% Indels: 0
DB: Gaps: 0
US-10-804-763-3 (1-198) x DB121562 (1-549)
Qy      18  AlaAlaArgProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGlu 37
Db      5  GCGCGCAGCCCGGAGCGTTCGGGGTGTCCGCGTGGATCGGACCTGGGAACCTGGGCGAG 64
Qy      38  ThrValGluLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeu 57
Db      65  ACAGTGGAGCTAAGTGCAGCGTGTCTGTCCACCCGACGCTGGGGCTGTCTGTGGCTC 124
Qy      58  PheGlnProArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLys 77
Db      125  TTTCCAGCGCGCGCGCGCGCGCGCGCTTCCTCTCTATACCTCTCTCCCAAAACAAG 184
Qy      78  ProLysAlaAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThr 97
Db      185  CCCAAGGCGCGCGGCGGCTGGACACCCAGCGGTTCTCGGCGAAGAGTTGGGGGACAC 244
Qy      98  PheValLeuThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAla 117
Db      245  TTCGTCTCTCACCTGAGCGACTTCGCGCGAGAGACGAGGGCTACTATTCTCTCGGCC 304
Qy      118  LeuSerAsnSerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysPro 137
Db      305  CTGAGCAACTCCATCATGTACTTCAGCACTTCGTCGGCGGTCTTCCTGCGAGGAAGCCC 364
Qy      138  ThrThrThrProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeu 157
Db      365  ACCACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 424
Qy      158  SerLeuArgProGluAlaCysArgProAlaAlaGlyGlyValGlyAlaGlyAsnArgArgVal 177
Db      425  TCCCTGGCGCCAGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGT 484
Qy      178  CysLysCysProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyr 197
Db      485  TGCAAAATGTCCCGCGCTGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 544
Qy      198  Val 198
Db      545  GTC 547
RESULT 7
AL552456
LOCUS
DEFINITION
AL552456 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSOD1070YG17 5-PRIME, mRNA sequence.

```


AL552456
 AL552456.3 GI:45857243
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 884)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31274271.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1670.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CSOD1070AD09QPI&c=1670.r.
 Location/Qualifiers
 1..884
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1070Y617"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,54e-71 Length: 884
 Score: 958.00 Matches: 195
 Percent Similarity: 98.5% Conservative: 0
 Best Local Similarity: 98.5% Mismatches: 3
 Query Match: 91.9% Indels: 3
 DB: 1 Gaps: 0
 US-10-804-763-3 (1-198) x AL552456 (1-884)
 QY 1 MetaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
 DB 71 ATGGCTTACAGTACCGCTTGTCTCTGCGCTGGCTTGTCTCCAGCGCCAGG 130
 QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyuThrValGlu 40
 DB 131 CG-AGCCAGTTCGGGGTTCGGCGTGGATCGGACCTGGAACTGGCGGAGACGTGGAG 189
 QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
 DB 190 CTGAGTGCAGGTCTGTCTCCAAACCGACGAGTGGGGTGTCTGTGGCTCTTCCAGCGC 249
 QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
 DB 250 CGCGGCGCGCGCGC-AGTCCCACTTCTCTCTATACCTCTCCAAAAACAAGCCAGGCG 308
 QY 81 AlaGluGlyLeuAspThrClnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
 DB 309 GCGGAGGGGCTGGACACCGCGGTCTCGGGCAAGAGTTGGGGACACCTTCTGTCTTC 368
 QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyTrpPheCysSerAlaLeuSerAsn 120
 DB 369 ACCCTGAGGCACTTCGGCGGAGAGAACGAGGGGCTACTATTCTGCTCGGCCCTGAGCAAC 428

QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
 DB 429 TCCATCATGTACTTCAGCCACTTCGTGCGGTCTTCTCGCAGCAACCCACC-ACGACG 487
 QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
 DB 488 CCAGCGCGGACCAACACCGCGGCCACCATCGCGTGCAGCCCTGTCCCTGGCG 547
 QY 161 ProGluAlaCysArgProAlaAlaGlyAlaGlyAlaGlyAsnArgArgValCysLysCys 180
 DB 548 CCAGAGGCGTCCGCGCAGCGCGGGGCGCAGCAACCCAGACGCTGTTTGCAATGT 607
 QY 181 ProArgProValValLysSerGlyAspLysProSerLeuSerAlaArgTyrVal 198
 DB 608 CCCCAGGCTGTGTGTCAAATCGGAGACAAGCCAGCCCTTCGCGCGAGATACGTC 661
 RESULT 8
 DA931234 838 bp mRNA linear EST 11-NOV-2005
 LOCUS DA931234 SPLEN1 Homo sapiens cDNA clone SPLEN1000141 5', mRNA
 DEFINITION DA931234
 VERSION DA931234
 ACCESSION DA931234.1 GI:82056788
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 838)
 Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
 Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaguri, H.,
 Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
 Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
 Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
 Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
 Diversification of Transcriptional Modulation: Large-scale
 Identification and Characterization of Putative Alternative
 Promoters of Human Genes
 Genome Res. 16 (1), 55-65 (2006)
 16344560
 Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology
 Developmental Organization, Japan); cDNA library construction:
 Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
 Research Association for Biotechnology (RAB) and Biotechnology
 Center, National Institute of Technology and Evaluation; 3'-end one
 pass sequencing: RAB.
 Location/Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
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 /clone_lib="SPLEN1"
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 FEATURES
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 ORIGIN
 Alignment Scores:
 Pred. No.: 4,23e-71 Length: 838
 Score: 952.50 Matches: 191
 Percent Similarity: 82.7% Conservative: 0
 Best Local Similarity: 82.7% Mismatches: 3
 Query Match: 91.3% Indels: 38
 DB: 9 Gaps: 1

US-10-804-763-3 (1-198) x DA931234 (1-838)

```

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArg 20
Db 89 ATGGCCTTACCACTGACCGCTTGCTCGCGCTGGCCTTGCTGCTCCACGCCGCCAGG 148
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 149 CCGAGCCAGTTCGGGTGCGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 208
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 209 CTGAAGTGCAGGTGCTGTCTCCACCCGACGTCGGCTGCTGCTGGTCTCTCCAGCCG 268
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db 269 CGCGGCCGCCGCCAGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAGCGC 328
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 329 GCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTGGGGACACCTTCGTCTC 388
QY 101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrPheCysSerAlaLeuSerAsn 120
Db 389 ACCCTGAGCGACTTCGCCGAGAGAACGAGGGCTACTATTCTGCTGGCCCTGAGCAAC 448
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 449 TCCATCATGTACTTCAGCCACTTCGTGCGCGTCTCTGCGCAGGAGGCCACACGAGC 508
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db 509 CCAGCGCCGCGACCAACACCGCGGCCACCATCGCTCGCAGGCCCTGTCCCTGCGC 568
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAla----- 171
Db 569 CCAGAGCGGTGCGCGCCAGCGCGGGGGCGCAGTGCAACAGAGGGGTGACTTCGCC 628
QY 171 ----- 171
Db 629 TGTGATATCTACATCTGGGGCGCCTTGGCGGGGACTTGTGGGGTCTCTCTCTGTCACTG 688
QY 172 -----GlyAsnArgArgArgValCysLysCysProArgPro 183
Db 689 GGTATCACCTTTACTGNAACTACAGGAACCGAAGACGTGTTGCAAAATGTCCTCGG-CT 747
QY 184 ValValLysSerGlyAspLysProSerLeuSer 194
Db 748 GTGGTCNAATCGGGAGACAAGCCAGCCCTTCG 780

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RESULT 9

BI820267
LOCUS 603036820F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5177885 5', linear EST 04-OCT-2001
DEFINITION mRNA sequence.

ACCESSION BI820267

VERSION BI820267.1 GI:15931817

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

1 (bases 1 to 882)

NIH-MGC <http://mgi.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLML1443 row: g column: 06

High quality sequence stop: 769.

FEATURES

Location/Qualifiers
source
1..882
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5177885"
/lab_host="DH10B"
/clone_lib="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27, and 1 male testis, age 69. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 5.5e-71 Length: 882
Score: 951.50 Matches: 193
Percent Similarity: 82.2% Conservatives: 1
Best Local Similarity: 81.8% Mismatches: 2
Query Match: 91.2% Indels: 40
DB: 2 Gaps: 1
US-10-804-763-3 (1-198) x BI820267 (1-882)

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QY 3 LeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuLeuHisAlaAlaArgProSer 22
Db 65 ATACCAGTGACCGCCTTGCTCTGCGCTGGCCTTGCTCTCCACGCCGCCAGCGCGAGC 124
QY 23 GlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGluLeuLys 42
Db 125 CAGTTCCGGGTGTCGCCGCTGGATCGGACCTGGGACCTGGGCGAGACAGTGGAGCTGAAG 184
QY 43 CysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnProArgGly 62
Db 185 TGCCAGGTGCTGCTGTCCAAACCCGACGTCGGCTGCTGCTGCTCTTCCAGCCGCCGCGC 244
QY 63 AlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAlaAlaGlu 82
Db 245 GCCGCCGCCAGTCCCACTTCTCTATACCTCTCCAAAACAAAGCCCAAGCGCGCGAG 304
QY 83 GlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeuThrLeu 102
Db 305 GGGCTGGACACCCAGCGGTCTCGGGCAAGAGGTGGGGGACACCTTCGTCTCACCCTG 364
QY 103 SerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerAsnSerIle 122
Db 365 AGCGACTTCCGCGGAGAGACGAGGGCTACTATTCTGCTCGGCCCTGAGCACTCATC 424
QY 123 MetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThrProAla 142
Db 425 ATGTACTTCAGCACTTCGTGCGGTCTTCTCCAGCGAAGCCCAACACGACGCGCGAGC 484
QY 143 ProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArgProGlu 162
Db 485 CGCGACCAACCAACACCGCGGCCACCATCGCGTCCGACGCCCTTGTCTTGGCCCGAG 544
QY 163 AlaCysArgProAlaAlaGlyGlyAla----- 171
Db 545 GGTGTCGCCGCCAGCGCGGGGGGCGCAGTGCACAGAGGGGCTGGACTTCGCCTGTGAT 604
QY 171 ----- 171

```

```

Db      605 ATCTACATCTGGGGCCCTTGGCCGGAGCTTGTGGGGTCTTCTCTCTGTCACCTGGTTAT 664
Qy      172 -----GlyAsnArgArgValCysLysCysProArgProValva 185
Db      665 CACCCTTTACTGCAACCAAGAACCGAAGACGTTGTCGAATGTCCTCCCGCCTGTGGT 724
Qy      185 llySer-GlyAspLys-ProSerLeuSerAlaArgTyrVal 198
Db      725 CAATCGGGGAGACAATGCCAGCCTTTCCGGCGAGATACGTC 766

RESULT 10
LOCUS   BI760947 780 bp mRNA linear EST 25-SEP-2001
DEFINITION 603043151F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183604 5',
mRNA sequence.
ACCESSION BI760947
VERSION   BI760947.1 GI:15752525
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11458 row: e column: 13
High quality sequence start: 4
High quality sequence stop: 756.
Location/Qualifiers
1..780
organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183604"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMW-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,26e-70 Length: 780
Score: 943.50 Matches: 195
Percent Similarity: 82.6% Conservative: 0
Best Local Similarity: 82.6% Mismatches: 2
Query Match: 90.5% Indels: 41
DB: 2 Gaps: 1

US-10-804-763-3 (1-198) x BI760947 (1-780)

Qy      1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db      67 ATGGCTTACCAGTACCGCCCTTGCTCCGCGCTTGCTGCTCCACGCCGCGCAG 126

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Qy      21 ProSerGlnPheArgValSerProLeuAspArgThrTyrAsnLeuGlyGluThrValGlu 40
Db      127 CCGAGCCAGTTCCTGGGTGTCGCCCTGGATCGGACCTGGAACTGGGGCGAGACAGTGGAG 186
Qy      41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTyrLeuPheGlnPro 60
Db      187 CTGAAGTGCCAGGTGCTGCTGTCCAAACCCGACGTGGGGCTGCTCGTGGCTCTTCCAGCGG 246
Qy      61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db      247 CGCGCGCGCGCGCCAGTCCACCTTCCTCTATACCTCTCCCAAAACAAGCCCAAGCGC 306
Qy      81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db      307 GCCAGGGGGCTGGGACACCCAGCGTCTCGGGCAAGAGTTGGGGGGACACCTTCGTCTC 366
Qy      101 ThrLeuSerAspPheArgArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db      367 ACCCTGAGCGACTTCCGCCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 426
Qy      121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db      427 TCCATCATGTACTTTCAGCCACTTCGTGCGGTCTTCTGCGCAGGAGGCCACCAACGAGC 486
Qy      141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db      487 CCAGCGCGCGACCAACCAACCCGCGGCCACCATCGCGTTCGACAGCCCTGTCCCTGGCG 546
Qy      161 ProGluLysCysArgProAlaAlaGlyGlyAlaGly----- 172
Db      547 CCAGAGGGCTGCCCGCCAGCGCGGGGGCGCAGT-GCACACGAGGGGGCTGGACTTCGC 605
Qy      172 ----- 172
Db      606 CTGTGATATCTACATCTGGGGCGCCCTTGGCGGGAGCTTGTGGGTCTTCTCTCTCACT 665
Qy      173 -----AsnArgArgArgValCysLysCysProArg 182
Db      666 TGGTTATCACCCTTTTACTGCAACACAGGAAACCGAAGACGTTGTTGCAAA-TGTCCCCGG 724
Qy      183 ProValValLysSerGlyAspLysProSerLeu-SerAlaArgTyr 197
Db      725 CTTGGTTCAAATCGGAGACACGCCAGCCTTTTCGGCGGAGATAC 770

RESULT 11
LOCUS   BX415859 1109 bp mRNA linear EST 03-MAY-2004
DEFINITION BX415859 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008YC20
5-PRIME, mRNA sequence.
ACCESSION BX415859
VERSION   BX415859.2 GI:46957661
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1109)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
On May 15, 2003 this sequence version replaced gi:30767593.
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
division of Invitrogen.
This sequence belongs to sequence cluster 1670.r

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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOCAP008BB10QPI&c=1670.r.

FEATURES

source

Location/Qualifiers

1. .1109

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSOCAP008YC20"

/tissue_type="THYMUS"

/clone_lib="Homo sapiens THYMUS"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 4,19e-69 Length: 1109
Score: 931.00 Matches: 194
Percent Similarity: 97.5% Conservative: 1
Best Local Similarity: 97.0% Mismatches: 3
Query Match: 89.3% Indels: 5
DB: 4 Gaps: 0

US-10-804-763-3 (1-198) x BX415859 (1-1109)

QY 1 MetAlaLeuProValThrAla-LeuLeuLeuProLeuAla-LeuLeuLeuHisAlaAlaA 20
DB 65 ATGGCTTACCAAGTACCCCTATGCTCTCGCGTGGCACTTGCTGCTCCAGCGGCCA 124
QY 20 rGProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValG 40
DB 125 GCGC-AGCCAGTTCGGGTGTGCGCGTGGACCTGGAACTGGGCGGAGACAGTGG 183
QY 40 luLeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnP 60
DB 184 AGCTGAAGTGCAGGCTGCTGTCCAAACCGACGTCGGCGTCTGCTGCTCCAGC 243
QY 60 roArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysA 80
DB 244 CGCGCGGCGCCGCC-AGTCCACCTTCTCTATACCTCTCCCAAAACAGCCCAAG 302
QY 80 laAlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValL 100
DB 303 CGGCGGAGGGCTGGACACCCAGCGGTTCTCGGGCAAGAGGTTGGGGACACCTTCGTC 362
QY 100 euThrLeuSerAspPheArgArgGluAsnGluGlyTyrTrpPheCysSerAlaLeuSerA 120
DB 363 TCACCTTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCA 422
QY 120 snSerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrT 140
DB 423 ACTCATCATGTACTTACGACCTTCGTCGGCTTCTCGCGCAAGACCCACC-ACCA 481
QY 140 hrProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuA 160
DB 482 CGCCAGCGCGGACCAACACCGCGGCCACCACCATCGCGTCGAGCCCTGTCCTGC 541
QY 160 rGProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArgValCysLysC 180
DB 542 GCCCAGAGCGTGCCTGGCGGCGGGGGGCGAGCAAGCGAATGTTTGGCAAT 601
QY 180 vsProArgProValLysSerGlyAspLysProSerLeuSerAlaAArgTyrVal 198
DB 602 GTCCCCGGCCTGTGTGTCAAATCGGAGAGCAAGCCAGCCCTTTCGGCGAGATACGTC 657

RESULT 12

DA943842

LOCUS

DA943842 SPLEN2 Homo sapiens cDNA clone SPLEN2018853 5', mRNA

DEFINITION

sequence.

ACCESSION

DA943842

VERSION

KEYWORDS

SOURCE

ORGANISM

DA943842.1 GI:82373467

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 566)

REFERENCE

AUTHORS

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kuehda,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.

Diversification of Transcriptional Modulation: Large-scale

Identification and Characterization of Putative Alternative

Promoters of Human Genes

Genome Res. 16 (1), 55-65 (2006)

16344560

Contact: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan): cDNA library construction. Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

source

Location/Qualifiers

1. 566

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="SPLEN2018853"

/tissue_type="spleen"

/clone_lib="SPLEN2"

/note="Vector: pME18SFL3"

ORIGIN

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Score: 928.00 Matches: 177
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 89.0% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DA943842 (1-566)

QY 1 MetAlaLeuProValThrAlaLeuLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
DB 36 ATGGCTTACCAAGTACCGCTTGTCTCTCGCGTGGCTTGTCTGCTCCACGCCGAG 95
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
DB 96 CCGAGCCAGTTCGGGTGTGCGCGTGGACCTGGAACTGGGGGAGACAGTGGAG 155
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
DB 156 CTGAAGTCCAGGTGCTGCTGTCCAAACCGAGCTGGGCTGCTGCTGCTTCCAGCCG 215
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
DB 216 CGCGCGCGCGCGCGAGTCCCACCTTCTCTCTATACCTCTCCCAAAACAAAGCCAGCG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
DB 276 GCCCGGGGGCTGGACACCCAGCGTTCCTGGGCAAGAGGTTGGGGGACACCTTCGCTC 335

Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

TITLE

JOURNAL

PUBMED

COMMENT

Genome Res. 16 (1), 55-65 (2006)
16344560

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

source

Location/Qualifiers

1..571
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SPLEN2030425"
/tissue_type="spleen"
/clone_lib="SPLEN2"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 9,61e-67 Length: 571
Score: 899.00 Matches: 172
Percent Similarity: 98.9% Conservatives: 1
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 86.2% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DA952710 (1-571)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 35 ATGGCTTACCAAGTACCGCTTCTCTCGCGCTGGCTTCTCTCCACCGCCAGG 94
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 95 CCGAGCCAGTTCGGGGTTCGGCGCTGGATCGGACCTGGAACTGGCGGAGACAGTGGAG 154
QY 41 LeuLysCysGlnValLeuSerAnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db 155 CTGAAGTGCAGGTGCTGTCTTCCACCGGAGCTGGGGTCTCTCTCCAGCGG 214
QY 61 ArgGlyAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAnLysProLysAla 80
Db 215 CGCGGGCGCGCCAGTCCGACCTTCTCTATACCTCTCCAAAACAGCCCGAGGG 274
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db 275 GCGGAGGGGCTGGACACCCAGCGGTTCCTCGGCAAGAGGTTGGGGGACACCTTCGCTCTC 334
QY 101 ThrLeuSerAspPheArgGluAnGluGlyTyrTyrPheCysSerAlaLeuSerAn 120
Db 335 ACCCTGAGCGACTTCGCGGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 394
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThrThr 140
Db 395 TCCATCATGTACTTCAGGCACATTCGCGCGGTCTTCTGCCAGCGAAGCCCAACAGCAGG 454
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160

Db 455 CCAGCGCGCGCGACCAACCGCGCCCAACATCGCTCGCAGCCCTGTCTCTCGCGC 514
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArg 175
Db 515 CCAGAGGCGTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 559

RESULT 15

DA826683

LOCUS

DEFINITION

DA826683 PERIC2 Homo sapiens cDNA clone PERIC2008112 5', mRNA

sequence.

ACCESSION

DA826683

VERSION

DA826683.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 576)

Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T., and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

TITLE

JOURNAL

PUBMED

COMMENT

Genome Res. 16 (1), 55-65 (2006)
16344560

Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES

source

Location/Qualifiers

1..576
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PERIC2008112"
/tissue_type="pericardium"
/clone_lib="PERIC2"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:

Pred. No.: 9,72e-67 Length: 576
Score: 899.00 Matches: 172
Percent Similarity: 98.9% Conservatives: 1
Best Local Similarity: 98.3% Mismatches: 2
Query Match: 86.2% Indels: 0
DB: 9 Gaps: 0

US-10-804-763-3 (1-198) x DA826683 (1-576)

QY 1 MetAlaLeuProValThrAlaLeuLeuProLeuAlaLeuLeuHisAlaAlaArg 20
Db 36 ATGGCTTACCAAGTACCGCTTCTCTCGCGCTGGCTTCTCTCCACCGCCAGG 95
QY 21 ProSerGlnPheArgValSerProLeuAspArgThrTrpAsnLeuGlyGluThrValGlu 40
Db 96 CCGAGCCAGTTCGGGGTTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 155

```
QY 41 LeuLysCysGlnValLeuLeuSerAsnProThrSerGlyCysSerTrpLeuPheGlnPro 60
Db |||||
156 CTGAAGTGCAGGTGCTGTGTCCAAACCGACGTCGGGCTGCTCGTGGCTCTTCCAGCG 215
QY 61 ArgGlyAlaAlaAlaSerProThrPheLeuLeuTyrLeuSerGlnAsnLysProLysAla 80
Db |||||
216 CGCGGCGCGCGCGCAGTCCACCTTCCTCTATACCTTCCCAAAACAAGCCCCAAGCG 275
QY 81 AlaGluGlyLeuAspThrGlnArgPheSerGlyLysArgLeuGlyAspThrPheValLeu 100
Db |||||
276 GCCGAGGGGCTGGACACCCAGCGGTCTCGGGCAAGAGTTGGGGGACACCTTCGTCTC 335
QY 101 ThrLeuSerAspPheArgGluAsnGluGlyTyrTyrPheCysSerAlaLeuSerAsn 120
Db |||||
336 ACCCTGAGCGACTTCGCGCGAGAGAACGAGGGCTACTATTCTGCTCGGCCCTGAGCAAC 395
QY 121 SerIleMetTyrPheSerHisPheValProValPheLeuProAlaLysProThrThr 140
Db |||||
396 TCCATCATGTACTTCAGCCACTTCGTGCGGCTTCTCGCCAGCGAAGCCACCACGACG 455
QY 141 ProAlaProArgProProThrProAlaProThrIleAlaSerGlnProLeuSerLeuArg 160
Db |||||
456 CCAGCGCGCGACCAACACCGCGGCCACCATCGCTCGCAGCCCCCTGTCTCTGCGC 515
QY 161 ProGluAlaCysArgProAlaAlaGlyGlyAlaGlyAsnArgArg 175
Db |||||
516 CCAGAGGCGTGC CGGCGCAGCGGGGGCGCGCAGTGCAACAGGAGG 560
```

Search completed: May 30, 2006, 06:51:27
Job time : 4306.33 secs

SEQUENCE COMPARISON 1 of 9/6/06

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2006, 21:45:26 ; Search time 2523 Seconds
(without alignments)
6248.218 Million cell updates/sec

Title: US-10-804-763-2
Perfect score: 2261
Sequence: 1 gaatacaggctccggcgccgg.....aaaaaaaaaaaaaaaaaaaaa 2261

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_8.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002as.*
 - 7: Geneseqn2002bs.*
 - 8: Geneseqn2003as.*
 - 9: Geneseqn2003bs.*
 - 10: Geneseqn2003cs.*
 - 11: Geneseqn2003ds.*
 - 12: Geneseqn2004as.*
 - 13: Geneseqn2004bs.*
 - 14: Geneseqn2005s.*
 - 15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 2261 | 100.0 | 2261 | 12 | ADP10406 |
| 2 | 2261 | 100.0 | 2261 | 13 | ADP10406 Reference |
| 3 | 2261 | 100.0 | 2261 | 13 | ADP10406 Reference |
| 4 | 2261 | 100.0 | 2261 | 13 | ADP10406 Reference |
| 5 | 2261 | 100.0 | 2261 | 14 | ADP10406 Reference |
| 6 | 2132.8 | 94.3 | 3048 | 12 | ADP10406 Reference |
| 7 | 2061.6 | 91.2 | 2134 | 12 | ADP10406 Reference |
| 8 | 2061.2 | 91.2 | 2123 | 10 | ADP10406 Reference |
| 9 | 2029 | 89.7 | 2150 | 13 | ADP10406 Reference |
| 10 | 2029 | 89.7 | 2150 | 13 | ADP10406 Reference |
| 11 | 2029 | 89.7 | 2150 | 14 | ADP10406 Reference |
| 12 | 1905 | 84.3 | 3518 | 14 | ADP10406 Reference |
| 13 | 1821 | 80.5 | 3476 | 14 | ADP10406 Reference |
| 14 | 1683 | 74.4 | 3407 | 14 | ADP10406 Reference |
| 15 | 1683 | 74.4 | 3743 | 14 | ADP10406 Reference |
| 16 | 1393 | 61.6 | 4392 | 14 | ADP10406 Reference |
| 17 | 1361.4 | 60.2 | 1729 | 12 | ADP10406 Reference |
| 18 | 1361.4 | 60.2 | 1729 | 13 | ADP10406 Reference |

| | | | | | |
|----|-------|------|------|----|----------|
| 19 | 1048 | 46.4 | 1060 | 2 | AAQ57986 |
| 20 | 1048 | 46.4 | 1060 | 10 | ADD25612 |
| 21 | 1048 | 46.4 | 1060 | 11 | AD131688 |
| 22 | 1048 | 46.4 | 1060 | 13 | ADS83755 |
| 23 | 761.4 | 33.7 | 773 | 3 | AAZ29002 |
| 24 | 744 | 32.9 | 744 | 14 | AED96294 |
| 25 | 708 | 31.3 | 708 | 2 | AAZ80967 |
| 26 | 708 | 31.3 | 708 | 8 | ABZ69260 |
| 27 | 708 | 31.3 | 708 | 13 | ADS92817 |
| 28 | 708 | 31.3 | 708 | 13 | ADS19462 |
| 29 | 708 | 31.3 | 708 | 14 | ADV42461 |
| 30 | 708 | 31.3 | 708 | 15 | AEF68357 |
| 31 | 704.8 | 31.2 | 708 | 8 | ABZ69262 |
| 32 | 676 | 29.9 | 727 | 10 | ADF90668 |
| 33 | 646.4 | 28.6 | 662 | 12 | ADN11772 |
| 34 | 644.4 | 28.5 | 1637 | 12 | ADN11778 |
| 35 | 644.4 | 28.5 | 2909 | 12 | ADN11779 |
| 36 | 610.4 | 27.0 | 708 | 13 | ADS92815 |
| 37 | 610.4 | 27.0 | 708 | 13 | ADS19461 |
| 38 | 610 | 27.0 | 610 | 12 | ADO41257 |
| 39 | 593 | 26.2 | 610 | 13 | ADU12274 |
| 40 | 586 | 25.9 | 599 | 12 | ADO41256 |
| 41 | 557.4 | 24.7 | 2001 | 13 | ADS92807 |
| 42 | 557.4 | 24.7 | 2001 | 13 | ADS19453 |
| 43 | 552 | 24.4 | 1891 | 13 | ADS92809 |
| 44 | 552 | 24.4 | 1891 | 13 | ADS19455 |
| 45 | 543 | 24.0 | 1131 | 3 | AAZ46253 |

ALIGNMENTS

RESULT 1

ADP10406

ID ADP10406 standard; DNA; 2261 BP.

XX ADP10406;

DT 12-AUG-2004 (first entry)

XX Reference mRNA sequences for marker probe #83.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.

OS Homo sapiens.

XX WO2004042346-A2.

XX 21-MAY-2004.

XX 24-APR-2003; 2003WO-US012946.

XX 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;

XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.

XX Claim 80; SEQ ID NO 415; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The

from plasmid only
yes
note

his page blank uspio
oiden